

A-527.ST25.txt  
SEQUENCE LISTING

<110> FEIGE, ULRICH  
LIU, CHUAN-FA  
CHEETHAM, JANET C.  
BOONE, THOMAS CHARLES

<120> MODIFIED PEPTIDES AS THERAPEUTIC AGENTS

<130> A-527

<140> 09/428,082

<141> 1999-10-22

<150> 60/105,371

<151> 1998-10-23

<160> 1133

<170> PatentIn version 3.1

<210> 1

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<212> DNA

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<222> (1)..(684)

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1 5 10 15	

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc	96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu	
20 25 30	

atg atc tcc ccg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc	144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser	
35 40 45	

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag	192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu	
50 55 60	

gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg	240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr	
65 70 75 80	

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat	288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn	
85 90 95	

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc	336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro	
100 105 110	

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag	384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln	
115 120 125	

gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc	432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val	
130 135 140	

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agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg      480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                      150                      155                      160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct      528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
165                      170                      175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc      576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
180                      185                      190

gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg      624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
195                      200                      205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg      672
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Ser Pro Gly Lys
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20                      25                      30

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Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
35                      40                      45

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His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
50                      55                      60

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Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                      70                      75                      80

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Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
85                      90                      95

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Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
100                      105                      110

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Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
115                      120                      125

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Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
130                      135                      140

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Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
145 150 155 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
165 170 175

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
195 200 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
210 215 220

Ser Pro Gly Lys  
225

<210> 3  
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<220>  
<221> misc\_feature  
<222> (18)..(18)  
<223> Methoxy-polyethylene glycol (5000 Dalton)-sulfoacetyl group attached to the sidechain.

<400> 3

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15

Gly Lys Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
20 25 30

Ala Ala Arg Ala  
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<220>  
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<223> Methoxy-polyethylene glycol (5000 Dalton)-succinimidyl group attached to the sidechain.

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 1 5 10 15

Gly Cys Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
 20 25 30

Ala Ala Arg Ala  
 35

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&lt;211&gt; 794

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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&lt;223&gt; Fc-TMP

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (39)..4779)

&lt;223&gt;

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 1 5

tgt cca cct tgt cca gct ccg gaa ctc ctg ggg gga ccg tca gtc ttc 104  
 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe  
 10 15 20

ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tc ggg acc cct 152  
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro  
 25 30 35

gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc 200  
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val  
 40 45 50

aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca 248  
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr  
 55 60 65 70

aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc 296  
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val  
 75 80 85

ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc 344  
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys  
 90 95 100

aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc 392  
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
 105 110 115

aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca 440  
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
 120 125 130

tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc 488  
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val



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135		140		145		150	
aaa ggc ttc tat	ccc agc gac atc gcc gtg gag tgg gag agc aat ggg						536
Lys Gly Phe Tyr	Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly	155		160		165	
cag ccg gag aac aac	tac aag acc acg cct ccc gtg ctg gac tcc gac						584
Gln Pro Glu Asn Asn	Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp	170		175		180	
ggc tcc ttc ttc ctc	tac agc aag ctc acc gtg gac aag agc agg tgg						632
Gly Ser Phe Phe Leu	Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp	185		190		195	
cag cag ggg aac gtc	ttc tca tgc tcc gtg atg cat gag gct ctg cac						680
Gln Gln Gly Asn Val	Phe Ser Cys Ser Val Met His Glu Ala Leu His	200		205		210	
aac cac tac acg cag	aag agc ctc tcc ctg tct ccg ggt aaa ggt gga						728
Asn His Tyr Thr Gln	Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly	215		220		225	230
ggt ggt ggt atc gaa	ggt ccg act ctg cgt cag tgg ctg gct gct cgt						776
Gly Gly Gly Ile Glu	Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg	235		240		245	
gct taatctcgag gatcc							794
Ala							

<210> 6  
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 1 5 10 15

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
 35 40 45

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
 65 70 75 80

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 85 90 95

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 100 105 110

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Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
115 120 125

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
145 150 155 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
165 170 175

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
195 200 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
210 215 220

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg  
225 230 235 240

Gln Trp Leu Ala Ala Arg Ala  
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1 5

tgt cca cct tgt cca gct ccg gaa ctc ctg ggg gga ccg tca gtc ttc 104  
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe  
10 15 20

ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct 152  
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro  
25 30 35

gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc 200  
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val  
40 45 50

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aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca      248
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
55                               60                               65                               70

aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc      296
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
75                               80                               85

ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc      344
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
90                               95                               100

aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc      392
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
105                              110                              115

aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca      440
Lys Ala Lys Gly Gln Pro Gln Glu Pro Gln Val Tyr Thr Leu Pro Pro
120                              125                              130

tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc      488
Ser Arg Asp Glu Leu Lys Asn Gln Val Ser Leu Thr Cys Leu Val
135                              140                              145                              150

aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg      536
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
155                              160                              165

cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac      584
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
170                              175                              180

ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg      632
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
185                              190                              195

cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac      680
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
200                              205                              210

aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa ggt gga      728
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly
215                              220                              225                              230

ggt ggt ggt atc gaa ggt ccg act ctg cgt cag tgg ctg gct gct cgt      776
Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg
235                              240                              245

gct ggt ggt gga ggt ggc ggc gga ggt att gag ggc cca acc ctt cgc      824
Ala Gly Gly Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg
250                              255                              260

caa tgg ctt gca gca cgc gcataatctc gaggatccg      861
Gln Trp Leu Ala Ala Arg
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<210> 8
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<212> PRT
<213> Artificial Sequence

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<400> 8

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1

5

15

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
35 40 45

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
65 70 75 80

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
85 90 95

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
100 105 110

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
115 120 125

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
145 150 155 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
165 170 175

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
195 200 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
210 215 220

Ser Pro Gly Lys Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg  
225 230 235 240

Gln Trp Leu Ala Ala Arg Ala Gly Gly Gly Gly Gly Gly Gly Ile  
245 250 255

Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg  
260 265

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215	220	225	230
aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca			776
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser			
	235	240	245
tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc			824
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser			
	250	255	260
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Leu Ser Leu Ser Pro Gly Lys			
	265		

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 1 5 10 15

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 20 25 30

Leu Ala Ala Arg Ala Gly Gly Gly Gly Gly Asp Lys Thr His Thr Cys  
 35 40 45

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu  
 50 55 60

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu  
 65 70 75 80

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys  
 85 90 95

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys  
 100 105 110

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu  
 115 120 125

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys  
 130 135 140

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys  
 145 150 155 160

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Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser  
165 170 175

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys  
180 185 190

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln  
195 200 205

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly  
210 215 220

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln  
225 230 235 240

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn  
245 250 255

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
260 265

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Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly Gly Gly Asp Lys  
10 15 20  
  
act cac aca tgt cca cct tgc cca gca cct gaa ctc ctg ggg gga ccg 152  
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro  
25 30 35  
  
tca gtt ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc 200  
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser  
40 45 50  
  
cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac 248  
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp  
55 60 65 70  
  
cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat 296  
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn  
75 80 85

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gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg      344
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
          90                      95                      100

gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag      392
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
          105                      110                      115

tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa      440
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
          120                      125                      130

acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc      488
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
          135                      140                      145

ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc      536
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
          155                      160                      165

tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag      584
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
          170                      175                      180

agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg      632
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
          185                      190                      195

gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag      680
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
          200                      205                      210

agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag      728
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
          215                      220                      225

gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt      776
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
          235                      240                      245

aaa taatggatcc      789
Lys

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<210> 12  
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<220>  
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20 25 30

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
35 40 45

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
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50

55

60

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
65 70 75 80

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr  
85 90 95

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp  
100 105 110

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
115 120 125

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
130 135 140

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys  
145 150 155 160

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
165 170 175

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
180 185 190

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
195 200 205

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
210 215 220

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
225 230 235 240

Leu Ser Leu Ser Pro Gly Lys  
245

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1 5 10

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1 5 10 15

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Ala Ala Arg Ala  
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<222> (39)..(797)

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Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe  
10 15 20

ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct 152  
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro  
25 30 35

gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc 200  
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val  
40 45 50

aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca 248  
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr  
55 60 65 70

aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc 296  
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val  
75 80 85

ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc 344  
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys  
90 95 100

aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc 392  
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
105 110 115

aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca 440  
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro

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aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly 155 160 165			536
cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp 170 175 180			584
ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp 185 190 195			632
cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His 200 205 210			680
aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa ggt gga Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly 215 220 225 230			728
ggt ggt ggt gga ggt act tac tct tgc cac ttc ggc ccg ctg act tgg Gly Gly Gly Gly Gly Thr Tyr Ser Cys His Phe Gly Pro Leu Thr Trp 235 240 245			776
gtt tgc aaa ccg cag ggt ggt taatctcgtg gatcc Val Cys Lys Pro Gln Gly Gly 250			812

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His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu 50 55 60
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr 65 70 75 80
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn 85 90 95

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Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
100 105 110

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
115 120 125

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
145 150 155 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
165 170 175

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
195 200 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
210 215 220

Ser Pro Gly Lys Gly Gly Gly Gly Gly Gly Thr Tyr Ser Cys His  
225 230 235 240

Phe Gly Pro Leu Thr Trp Val Cys Lys Pro Gln Gly Gly  
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Cys His Phe Gly Pro Leu Thr Trp Val Cys Lys Pro Gln Gly Gly Gly  
10 15 20

gga ggc ggg ggg gac aaa act cac aca tgt cca cct tgc cca gca cct 152  
Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
25 30 35

A-527.ST25.txt

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gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg	248
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val	
55 60 65 70	
gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac	296
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp	
75 80 85	
ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac	344
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr	
90 95 100	
aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac	392
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp	
105 110 115	
tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc	440
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu	
120 125 130	
cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga	488
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg	
135 140 145 150	
gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag	536
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys	
155 160 165	
aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac	584
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp	
170 175 180	
atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag	632
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys	
185 190 195	
acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc	680
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser	
200 205 210	
aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca	728
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser	
215 220 225 230	
tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc	776
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser	
235 240 245	
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Leu Ser Leu Ser Pro Gly Lys	
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Lys Pro Gln Gly Gly Gly Gly Gly Gly Gly Gly Asp Lys Thr His Thr Cys  
20 25 30

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu  
35 40 45

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu  
50 55 60

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys  
65 70 75 80

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys  
85 90 95

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu  
100 105 110

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys  
115 120 125

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys  
130 135 140

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser  
145 150 155 160

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys  
165 170 175

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln  
180 185 190

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly  
195 200 205

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln  
210 215 220

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn  
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&lt;223&gt; EMP-EMP-Fc

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&lt;222&gt; (41)..(871)

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1      5

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Ser Cys His Phe Gly Pro Leu Thr Trp Val Cys Lys Pro Gln Gly Gly
10      15      20

ggc ggc ggc ggc ggt ggt acc tat tcc tgt cat ttt ggc ccg ctg acc      151
Gly Gly Gly Gly Gly Gly Thr Tyr Ser Cys His Phe Gly Pro Leu Thr
25      30      35

tgg gta tgt aag cca caa ggg ggt ggg gga ggc ggg ggg gac aaa act      199
Trp Val Cys Lys Pro Gln Gly Gly Gly Gly Gly Gly Gly Asp Lys Thr
40      45      50

cac aca tgt cca cct tgc cca gca cct gaa ctc ctg ggg gga ccg tca      247
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
55      60      65

gtt ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg      295
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
70      75      80      85

acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct      343
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
90      95      100

gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc      391
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
105      110      115

aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc      439
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
120      125      130

agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac      487
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
135      140      145

aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc      535
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
150      155      160      165

atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg      583
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
170      175      180

ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc      631
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
185      190      195

ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc      679
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
200      205      210

aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac      727
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp

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225

ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa 871  
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35 40 45

Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu  
50 55 60

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
65 70 75 80

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
85 90 95

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
100 105 110

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser  
115 120 125

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
130 135 140

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
145 150 155 160

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro



165

170

175

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln  
 180 185 190

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
 195 200 205

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
 210 215 220

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
 225 230 235 240

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
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Leu Ser Pro Gly Lys  
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 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe  
 10 15 20

ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct 152  
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro  
 25 30 35

gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc 200  
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val  
 40 45 50

aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca 248  
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr  
 55 60 65 70

aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc 296  
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val

A-527.ST25.txt

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Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser					
		105					110					115								
aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	cct	cca	440				
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro					
	120					125					130									
tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	ctg	gtc	488				
Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val					
135					140					145					150					
aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	agc	aat	ggg	536				
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly					
				155					160					165						
cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	gtg	ctg	gac	tcc	gac	584				
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp					
			170					175					180							
ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	agc	agg	tgg	632				
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp					
		185					190					195								
cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct	ctg	cac	680				
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His					
	200					205					210									
aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	ccg	ggg	aaa	ggg	gga	728				
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	Gly	Gly					
215					220					225					230					
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Gly	Gly	Gly	Gly	Gly	Thr	Tyr	Ser	Cys	His	Phe	Gly	Pro	Leu	Thr	Trp					
				235					240					245						
gtt	tgc	aaa	ccg	cag	ggg	ggc	ggc	ggc	ggc	ggc	ggg	ggg	acc	tat	tcc	824				
Val	Cys	Lys	Pro	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Thr	Tyr	Ser					
			250				255						260							
tgt	cat	ttt	ggc	ccg	ctg	acc	tgg	gta	tgt	aag	cca	caa	ggg	ggg		869				
Cys	His	Phe	Gly	Pro	Leu	Thr	Trp	Val	Cys	Lys	Pro	Gln	Gly	Gly						
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885

<210> 22  
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<220>  
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Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 Page 22

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
 35 40 45  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 50 55 60  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
 65 70 75 80  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 85 90 95  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 100 105 110  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
 115 120 125  
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
 130 135 140  
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
 145 150 155 160  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
 165 170 175  
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
 180 185 190  
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
 195 200 205  
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
 210 215 220  
 Ser Pro Gly Lys Gly Gly Gly Gly Gly Gly Thr Tyr Ser Cys His  
 225 230 235 240  
 Phe Gly Pro Leu Thr Trp Val Cys Lys Pro Gln Gly Gly Gly Gly Gly  
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 ctccctgagta ggacaaatcc gccgggagcg gatttgaacg ttgcgaagca acggccccga 180  
 ggggtggcggg caggacgcc gccataaact gccaggcatc aaattaagca gaaggccatc 240  
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 ccttcgcatg cccacgctaa acattctttt tctcttttg ttaaategtt gtttgattta 540  
 ttatttgcta tattttattt tcgataatta tcaactagag aaggaacaat taatggtatg 600  
 ttcatacacg catgtaaaaa taaactatct atatagttgt ctttctctga atgtgcaaaa 660  
 ctaagcattc cgaagccatt attagcagta tgaataggga aactaaaccc agtgataaga 720  
 cctgatgatt tcgcttcttt aattacattt ggagattttt tatttacagc attgttttca 780  
 aatatattcc aattaatcgg tgaatgattg gagttagaat aatctactat aggatcatat 840  
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 gaaatatcag atttaaccat agaattgagga taaatgatcg cgagtaaata atattcacia 960  
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<210> 24  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

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&lt;210&gt; 25

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TPO-MIMETIC PEPTIDE

&lt;400&gt; 25

Ile Glu Gly Pro Thr Leu Arg Glu Trp Leu Ala Ala Arg Ala  
 1 5 10

&lt;210&gt; 26

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TPO-MIMETIC PEPTIDE

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (14)..(14)

&lt;223&gt; At position 14, amino acid linker to an identical sequence

&lt;400&gt; 26

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala  
 1 5 10

&lt;210&gt; 27

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TPO-MIMETIC PEPTIDE

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (14)..(14)

&lt;223&gt; At position 14, amino acid linker to an identical sequence

&lt;400&gt; 27

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Lys Ala  
 1 5 10

&lt;210&gt; 28

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TPO-MIMETIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (9)..(9)  
 <223> At position 9 disulfide linkage to position 9 of an identical sequence -

<220>  
 <221> misc\_feature  
 <222> (14)..(14)  
 <223> At position 14, amino acid linker to an identical sequence

<400> 28

Ile Glu Gly Pro Thr Leu Arg Gln Cys Leu Ala Ala Arg Ala  
 1 5 10

<210> 29  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (16)..(16)  
 <223> Position 16 bromoacetyl group linked to sidechain

<220>  
 <221> misc\_feature  
 <222> (14)..(14)  
 <223> At position 14, amino acid linker attached N-to-C to Lys and to a nother linker and an identical sequence

<400> 29

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala  
 1 5 10

<210> 30  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (16)..(16)  
 <223> Position 16 polyethylene glycol linked to sidechain

<220>  
 <221> misc\_feature  
 <222> (14)..(14)  
 <223> At position 14, amino acid linker attached N-to-C to Lys and to a nother linker and an identical sequence

&lt;400&gt; 30

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala  
 1 5 10

&lt;210&gt; 31

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TPO-MIMETIC PEPTIDE

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (9)..(9)

&lt;223&gt; Position 9 disulfide bond to residue 9 of a separate identical sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (14)..(14)

&lt;223&gt; At position 14, amino acid linker to an identical sequence

&lt;400&gt; 31

Ile Glu Gly Pro Thr Leu Arg Gln Cys Leu Ala Ala Arg Ala  
 1 5 10

&lt;210&gt; 32

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TPO-MIMETIC PEPTIDE

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (14)..(14)

&lt;223&gt; At position 14, amino acid linker attachment site

&lt;400&gt; 32

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala  
 1 5 10

&lt;210&gt; 33

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TPO MIMETIC PEPTIDE

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (6, 7 and)..(8)

&lt;223&gt; Xaa = any amino acid

&lt;400&gt; 33

Val Arg Asp Gln Ile Xaa Xaa Xaa Leu  
1 5

<210> 34 -  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC PEPTIDE

<400> 34

Thr Leu Arg Glu Trp Leu  
1 5

<210> 35  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC PEPTIDE

<400> 35

Gly Arg Val Arg Asp Gln Val Ala Gly Trp  
1 5 10

<210> 36  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC PEPTIDE

<400> 36

Gly Arg Val Lys Asp Gln Ile Ala Gln Leu  
1 5 10

<210> 37  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC PEPTIDE

<400> 37

Gly Val Arg Asp Gln Val Ser Trp Ala Leu  
1 5 10

<210> 38  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC PEPTIDE



&lt;400&gt; 38

Glu	Ser	Val	Arg	Glu	Gln	Val	Met	Lys	Tyr
1				5					10

&lt;210&gt; 39

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TPO-MIMETIC PEPTIDE

&lt;400&gt; 39

Ser	Val	Arg	Ser	Gln	Ile	Ser	Ala	Ser	Leu
1				5					10

&lt;210&gt; 40

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TPO-MIMETIC PEPTIDE

&lt;400&gt; 40

Gly	Val	Arg	Glu	Thr	Val	Tyr	Arg	His	Met
1				5					10

&lt;210&gt; 41

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TPO-MIMETIC PEPTIDE

&lt;400&gt; 41

Gly	Val	Arg	Glu	Val	Ile	Val	Met	His	Met	Leu
1				5						10

&lt;210&gt; 42

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TPO-MIMETIC PEPTIDE

&lt;400&gt; 42

Gly	Arg	Val	Arg	Asp	Gln	Ile	Trp	Ala	Ala	Leu
1				5						10

&lt;210&gt; 43

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<400> 43

Ala Gly Val Arg Asp Gln Ile Leu Ile Trp Leu  
 1 5 10

<210> 44  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<400> 44

Gly Arg Val Arg Asp Gln Ile Met Leu Ser Leu  
 1 5 10

<210> 45  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (8)..(10)  
 <223> Xaa = any amino acid

<400> 45

Gly Arg Val Arg Asp Gln Ile Xaa Xaa Xaa Leu  
 1 5 10

<210> 46  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<400> 46

Cys Thr Leu Arg Gln Trp Leu Gln Gly Cys  
 1 5 10

<210> 47  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<400> 47

Cys Thr Leu Gln Glu Phe Leu Glu Gly Cys  
 Page 30

1 5

<210> 48  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC PEPTIDE

<400> 48

Cys Thr Arg Thr Glu Trp Leu His Gly Cys  
1 5 10

<210> 49  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC PEPTIDE

<400> 49

Cys Thr Leu Arg Glu Trp Leu His Gly Gly Phe Cys  
1 5 10

<210> 50  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC PEPTIDE

<400> 50

Cys Thr Leu Arg Glu Trp Val Phe Ala Gly Leu Cys  
1 5 10

<210> 51  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC PEPTIDE

<400> 51

Cys Thr Leu Arg Gln Trp Leu Ile Leu Leu Gly Met Cys  
1 5 10

<210> 52  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC PEPTIDE

<400> 52

Cys Thr Leu Ala Glu Phe Leu Ala Ser Gly Val Glu Gln Cys  
 1 5 10

<210> 53  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<400> 53

Cys Ser Leu Gln Glu Phe Leu Ser His Gly Gly Tyr Val Cys  
 1 5 10

<210> 54  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<400> 54

Cys Thr Leu Arg Glu Phe Leu Asp Pro Thr Thr Ala Val Cys  
 1 5 10

<210> 55  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<400> 55

Cys Thr Leu Lys Glu Trp Leu Val Ser His Glu Val Trp Cys  
 1 5 10

<210> 56  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (8)..(9)  
 <223> Xaa = any amino acid

<400> 56

Cys Thr Leu Arg Glu Trp Leu Xaa Xaa Cys  
 1 5 10

<210> 57

<211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (8)..(10)  
 <223> Xaa = any amino acid

<400> 57

Cys Thr Leu Arg Glu Trp Leu Xaa Xaa Xaa Cys  
 1 5 10

<210> 58  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (8)..(11)  
 <223> Xaa = any amino acid

<400> 58

Cys Thr Leu Arg Glu Trp Leu Xaa Xaa Xaa Xaa Cys  
 1 5 10

<210> 59  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (8)..(12)  
 <223> Xaa = any amino acid

<400> 59

Cys Thr Leu Arg Glu Trp Leu Xaa Xaa Xaa Xaa Xaa Cys  
 1 5 10

<210> 60  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<220>

<221> misc\_feature  
 <222> (8)..(13)  
 <223> Xaa = any amino acid

<400> 60

Cys Thr Leu Arg Glu Trp Leu Xaa Xaa Xaa Xaa Xaa Xaa Cys  
 1 5 10

<210> 61  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<400> 61

Arg Glu Gly Pro Thr Leu Arg Gln Trp Met  
 1 5 10

<210> 62  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<400> 62

Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala  
 1 5 10

<210> 63  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<400> 63

Glu Arg Gly Pro Phe Trp Ala Lys Ala Cys  
 1 5 10

<210> 64  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<400> 64

Arg Glu Gly Pro Arg Cys Val Met Trp Met  
 1 5 10

<210> 65

<211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<400> 65

Cys Gly Thr Glu Gly Pro Thr Leu Ser Thr Trp Leu Asp Cys  
 1 5 10

<210> 66  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<400> 66

Cys Glu Gln Asp Gly Pro Thr Leu Leu Glu Trp Leu Lys Cys  
 1 5 10

<210> 67  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<400> 67

Cys Glu Leu Val Gly Pro Ser Leu Met Ser Trp Leu Thr Cys  
 1 5 10

<210> 68  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<400> 68

Cys Leu Thr Gly Pro Phe Val Thr Gln Trp Leu Tyr Glu Cys  
 1 5 10

<210> 69  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<400> 69

Cys Arg Ala Gly Pro Thr Leu Leu Glu Trp Leu Thr Leu Cys  
 1 5 10

<210> 70  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<400> 70

Cys Ala Asp Gly Pro Thr Leu Arg Glu Trp Ile Ser Phe Cys  
 1 5 10

<210> 71  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (2 )..(12)  
 <223> Xaa = any amino acid

<400> 71

Cys Xaa Glu Gly Pro Thr Leu Arg Glu Trp Leu Xaa Cys  
 1 5 10

<210> 72  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (2, 3 )..(13)  
 <223> Xaa = any amino acid

<400> 72

Cys Xaa Xaa Glu Gly Pro Thr Leu Arg Glu Trp Leu Xaa Cys  
 1 5 10

<210> 73  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (2, 12 )..(13)  
 <223> Xaa = any amino acid



&lt;400&gt; 73

Cys Xaa Glu Gly Pro Thr Leu Arg Glu Trp Leu Xaa Xaa Cys  
 1 5 10

<210> 74  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (2, 3, 13 )..(14)  
 <223> Xaa = any amino acid

&lt;400&gt; 74

Cys Xaa Xaa Glu Gly Pro Thr Leu Arg Glu Trp Leu Xaa Xaa Cys  
 1 5 10 15

<210> 75  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

&lt;400&gt; 75

Gly Gly Cys Thr Leu Arg Glu Trp Leu His Gly Gly Phe Cys Gly Gly  
 1 5 10 15

<210> 76  
 <211> 18  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

&lt;400&gt; 76

Gly Gly Cys Ala Asp Gly Pro Thr Leu Arg Glu Trp Ile Ser Phe Cys  
 1 5 10 15

Gly Gly

<210> 77  
 <211> 19  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDE

&lt;400&gt; 77

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Gly Asn Ala Asp Gly Pro Thr Leu Arg Gln Trp Leu Glu Gly Arg Arg  
1 5 10 15

Pro Lys Asn -

<210> 78  
<211> 19  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC PEPTIDE

<400> 78

Leu Ala Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu His Gly Asn Gly  
1 5 10 15

Arg Asp Thr

<210> 79  
<211> 19  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC PEPTIDE

<400> 79

His Gly Arg Val Gly Pro Thr Leu Arg Glu Trp Lys Thr Gln Val Ala  
1 5 10 15

Thr Lys Lys

<210> 80  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC PEPTIDE

<400> 80

Thr Ile Lys Gly Pro Thr Leu Arg Gln Trp Leu Lys Ser Arg Glu His  
1 5 10 15

Thr Ser

<210> 81  
<211> 18  
<212> PRT  
<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; TPO-MIMETIC PEPTIDE

&lt;400&gt; 81

Ile Ser Asp Gly Pro Thr Leu Lys Glu Trp Leu Ser Val Thr Arg Gly  
 1 5 10 15

Ala Ser

&lt;210&gt; 82

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TPO MIMETIC PEPTIDE

&lt;400&gt; 82

Ser Ile Glu Gly Pro Thr Leu Arg Glu Trp Leu Thr Ser Arg Thr Pro  
 1 5 10 15

His Ser

&lt;210&gt; 83

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; EPO-MIMETIC PEPTIDE

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (2, 4, 5, 8, 11 )..(13)

&lt;223&gt; Xaa = any amino acid

&lt;400&gt; 83

Tyr Xaa Cys Xaa Xaa Gly Pro Xaa Thr Trp Xaa Cys Xaa Pro  
 1 5 10

&lt;210&gt; 84

&lt;211&gt; 28

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; EPO-MIMETIC PEPTIDE

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (2, 4, 5, 8, 11, 13, 16, 18, 19, 22, 25 )..(27)

&lt;223&gt; Xaa = any amino acid

&lt;400&gt; 84

Tyr Xaa Cys Xaa Xaa Gly Pro Xaa Thr Trp Xaa Cys Xaa Pro Tyr Xaa  
 Page 39

1 5 15

Cys Xaa Xaa Gly Pro Xaa Thr Trp Xaa Cys Xaa Pro  
20 25

<210> 85  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> EPO-MIMETIC PEPTIDE

<220>  
<221> misc\_feature  
<222> (14)..(14)  
<223> At position 14, amino acid linker to an identical sequence

<220>  
<221> misc\_feature  
<222> (2, 4, 5, 8, 11)..(13)  
<223> Xaa = any amino acid

<400> 85

Tyr Xaa Cys Xaa Xaa Gly Pro Xaa Thr Trp Xaa Cys Xaa Pro  
1 5 10

<210> 86  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> EPO-MIMETIC PEPTIDE

<220>  
<221> misc\_feature  
<222> (2, 4, 5, 8, 11 )..(13)  
<223> Xaa = any amino acid

<400> 86

Tyr Xaa Cys Xaa Xaa Gly Pro Xaa Thr Trp Xaa Cys Xaa Pro  
1 5 10

<210> 87  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> EPO-MIMETIC PEPTIDE

<400> 87

Gly Gly Thr Tyr Ser Cys His Phe Gly Pro Leu Thr Trp Val Cys Lys  
1 5 10 15

Pro Gln Gly Gly

20

<210> 88  
 <211> 20  
 <212> PRT -  
 <213> Artificial Sequence

<220>  
 <223> EPO-MIMETIC PEPTIDE

<400> 88

Gly Gly Asp Tyr His Cys Arg Met Gly Pro Leu Thr Trp Val Cys Lys  
 1 5 10 15

Pro Leu Gly Gly  
 20

<210> 89  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> EPO-MIMETIC PEPTIDE

<400> 89

Gly Gly Val Tyr Ala Cys Arg Met Gly Pro Ile Thr Trp Val Cys Ser  
 1 5 10 15

Pro Leu Gly Gly  
 20

<210> 90  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> EPO-MIMETIC PEPTIDE

<400> 90

Val Gly Asn Tyr Met Cys His Phe Gly Pro Ile Thr Trp Val Cys Arg  
 1 5 10 15

Pro Gly Gly Gly  
 20

<210> 91  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> EPO-MIMETIC PEPTIDE

<400> 91

Gly Gly Leu Tyr Leu Cys Arg Phe Gly Pro Val Thr Trp Asp Cys Gly  
 Page 41

1 5 15

Tyr Lys Gly Gly  
20

<210> 92  
<211> 40  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> EPO-MIMETIC PEPTIDE

<400> 92

Gly Gly Thr Tyr Ser Cys His Phe Gly Pro Leu Thr Trp Val Cys Lys  
1 5 10 15

Pro Gln Gly Gly Gly Gly Thr Tyr Ser Cys His Phe Gly Pro Leu Thr  
20 25 30

Trp Val Cys Lys Pro Gln Gly Gly  
35 40

<210> 93  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> EPO-MIMETIC PEPTIDE

<220>  
<221> misc\_feature  
<222> (20)..(20)  
<223> Position 20, amino acid linker to an identical sequence

<400> 93

Gly Gly Thr Tyr Ser Cys His Phe Gly Pro Leu Thr Trp Val Cys Lys  
1 5 10 15

Pro Gln Gly Gly  
20

<210> 94  
<211> 23  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> EPO-MIMETIC PEPTIDE

<400> 94

Gly Gly Thr Tyr Ser Cys His Phe Gly Pro Leu Thr Trp Val Cys Lys  
1 5 10 15

Pro Gln Gly Gly Ser Ser Lys

20

<210> 95  
 <211> 46  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> EPO-MIMETIC PEPTIDE

<400> 95

Gly Gly Thr Tyr Ser Cys His Phe Gly Pro Leu Thr Trp Val Cys Lys  
 1 5 10 15

Pro Gln Gly Gly Ser Ser Lys Gly Gly Thr Tyr Ser Cys His Phe Gly  
 20 25 30

Pro Leu Thr Trp Val Cys Lys Pro Gln Gly Gly Ser Ser Lys  
 35 40 45

<210> 96  
 <211> 23  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> EPO-MIMETIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (23)..(23)  
 <223> Position 23, amino acid linker to an identical sequence

<400> 96

Gly Gly Thr Tyr Ser Cys His Phe Gly Pro Leu Thr Trp Val Cys Lys  
 1 5 10 15

Pro Gln Gly Gly Ser Ser Lys  
 20

<210> 97  
 <211> 22  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> EPO-MIMETIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (22)..(22)  
 <223> Position 22 linked through epsilon amine to lysyl, which is linked to a separate identical sequence through that sequence's alpha amine

<400> 97

Gly Gly Thr Tyr Ser Cys His Phe Gly Pro Leu Thr Trp Val Cys Lys  
 Page 43

1 5 A-527.ST25.txt 15  
10

Pro Gln Gly Gly Ser Ser  
20

-

<210> 98  
<211> 23  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> EPO-MIMETIC PEPTIDE

<220>  
<221> misc\_feature  
<222> (23)..(23)  
<223> At position 23 biotin linked to the sidechain through a linker

<400> 98

Gly Gly Thr Tyr Ser Cys His Phe Gly Pro Leu Thr Trp Val Cys Lys  
1 5 10 15

Pro Gln Gly Gly Ser Ser Lys  
20

<210> 99  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> G-CSF-MIMETIC PEPTIDE

<220>  
<221> misc\_feature  
<222> (4)..(4)  
<223> At position 4 disulfide bond to residue 4 of a separate identical sequence

<400> 99

Glu Glu Asp Cys Lys  
1 5

<210> 100  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> G-CSF-MIMETIC PEPTIDE

<220>  
<221> misc\_feature  
<222> (4)..(4)  
<223> At position 4, Xaa is an isoteric ethylene spacer linked to a separate identical sequence

<400> 100



Glu Glu Asp Xaa Lys  
1 5

<210> 101 -  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> G-CSF-MIMETIC PEPTIDE

<220>  
<221> misc\_feature  
<222> (1)..(1)  
<223> Position 1, Xaa is a pyroglutamic acid residue

<220>  
<221> misc\_feature  
<222> (5)..(5)  
<223> Position 5, Xaa is an isoteric ethylene spacer linked to a separate identical sequence.

<400> 101

Xaa Gly Glu Asp Xaa Lys  
1 5

<210> 102  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> G-CSF-MIMETIC PEPTIDE

<220>  
<221> misc\_feature  
<222> (1)..(1)  
<223> Position 1, Xaa is a picolinic acid residue

<220>  
<221> misc\_feature  
<222> (4)..(4)  
<223> Position 4, Xaa is an isoteric ethylene spacer linked to a separate identical sequence.

<400> 102

Xaa Ser Asp Xaa Lys  
1 5

<210> 103  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> G-CSF-MIMETIC PEPTIDE

<220>

<221> misc\_feature  
 <222> (5)..(5)  
 <223> At position 5, amino acid linker to an identical sequence

<400> 103 -

Glu Glu Asp Cys Lys  
 1 5

<210> 104  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> G-CSF-MIMETIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (5)..(5)  
 <223> At position 5, amino acid linker to an identical sequence

<220>  
 <221> misc\_feature  
 <222> (4)..(4)  
 <223> Xaa = any amino acid

<400> 104

Glu Glu Asp Xaa Lys  
 1 5

<210> 105  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ANTIVIRAL (HBV)

<400> 105

Leu Leu Gly Arg Met Lys  
 1 5

<210> 106  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TNF ANTAGONIST PEPTIDE

<400> 106

Tyr Cys Phe Thr Ala Ser Glu Asn His Cys Tyr  
 1 5 10

<210> 107  
 <211> 11  
 <212> PRT

<213> Artificial Sequence

<220>

<223> TNF ANTAGONIST PEPTIDE

<400> 107 -

Tyr Cys Phe Thr Asn Ser Glu Asn His Cys Tyr  
1 5 10

<210> 108

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> TNF ANTAGONIST PEPTIDE

<400> 108

Tyr Cys Phe Thr Arg Ser Glu Asn His Cys Tyr  
1 5 10

<210> 109

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> TNF ANTAGONIST PEPTIDE

<400> 109

Phe Cys Ala Ser Glu Asn His Cys Tyr  
1 5

<210> 110

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> TNF ANTAGONIST PEPTIDE

<400> 110

Tyr Cys Ala Ser Glu Asn His Cys Tyr  
1 5

<210> 111

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> TNF ANTAGONIST PEPTIDE

<400> 111

Phe Cys Asn Ser Glu Asn His Cys Tyr  
1 5

<210> 112

<211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TNF ANTAGONIST PEPTIDE

<400> 112

Phe Cys Asn Ser Glu Asn Arg Cys Tyr  
 1 5

<210> 113  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TNF ANTAGONIST PEPTIDE

<400> 113

Phe Cys Asn Ser Val Glu Asn Arg Cys Tyr  
 1 5 10

<210> 114  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TNF ANTAGONIST PEPTIDE

<400> 114

Tyr Cys Ser Gln Ser Val Ser Asn Asp Cys Phe  
 1 5 10

<210> 115  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TNF ANTAGONIST PEPTIDE

<400> 115

Phe Cys Val Ser Asn Asp Arg Cys Tyr  
 1 5

<210> 116  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TNF ANTAGONIST PEPTIDE

<400> 116

Tyr Cys Arg Lys Glu Leu Gly Gln Val Cys Tyr  
 1 5 10

<210> 117  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TNF ANTAGONIST PEPTIDE

<400> 117

Tyr Cys Lys Glu Pro Gly Gln Cys Tyr  
 1 5

<210> 118  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TNF ANTAGONIST PEPTIDE

<400> 118

Tyr Cys Arg Lys Glu Met Gly Cys Tyr  
 1 5

<210> 119  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TNF ANTAGONIST PEPTIDE

<400> 119

Phe Cys Arg Lys Glu Met Gly Cys Tyr  
 1 5

<210> 120  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TNF ANTAGONIST PEPTIDE

<400> 120

Tyr Cys Trp Ser Gln Asn Leu Cys Tyr  
 1 5

<210> 121  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TNF ANTAGONIST PEPTIDE

<400> 121

Tyr Cys Glu Leu Ser Gln Tyr Leu Cys Tyr

1 5

<210> 122  
<211> 9  
<212> PRT -  
<213> Artificial Sequence

<220>  
<223> TNF ANTAGONIST PEPTIDE

<400> 122

Tyr Cys Trp Ser Gln Asn Tyr Cys Tyr  
1 5

<210> 123  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TNF ANTAGONIST PEPTIDE

<400> 123

Tyr Cys Trp Ser Gln Tyr Leu Cys Tyr  
1 5

<210> 124  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> EPO-MIMETIC PEPTIDE

<220>  
<221> misc\_feature  
<222> (1)..(1)  
<223> Xaa (Pos1) can be C, A, a-amino-g-bromobutyric acid or Hoc.

<220>  
<221> misc\_feature  
<222> (2)..(2)  
<223> Xaa can be R, H, L or W.

<220>  
<221> misc\_feature  
<222> (3)..(3)  
<223> Xaa can be M, F or I.

<220>  
<221> misc\_feature  
<222> (6)..(6)  
<223> Xaa can be any one of the 20 L-amino acids or the stereoisomeric D-amino acids.

<220>  
<221> misc\_feature  
<222> (9)..(9)  
<223> Xaa can be D, E, I, L or V.

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Xaa can-be a-amino-g-bromobutyric acid or Hoc, provided that either Xaa (Pos1) or Xaa (Pos10) is C or Hoc.

<400> 124

Xaa Xaa Xaa Gly Pro Xaa Thr Trp Xaa Xaa  
 1 5 10

<210> 125  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> CTLA4-MIMETIC

<400> 125

Gly Phe Val Cys Ser Gly Ile Phe Ala Val Gly Val Gly Arg Cys  
 1 5 10 15

<210> 126  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> CTLA4-MIMETIC

<400> 126

Ala Pro Gly Val Arg Leu Gly Cys Ala Val Leu Gly Arg Tyr Cys  
 1 5 10 15

<210> 127  
 <211> 27  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> C3B ANTAGONIST

<400> 127

Ile Cys Val Val Gln Asp Trp Gly His His Arg Cys Thr Ala Gly His  
 1 5 10 15

Met Ala Asn Leu Thr Ser His Ala Ser Ala Ile  
 20 25

<210> 128  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> C3B ANTAGONIST

&lt;400&gt; 128

Ile	Cys	Val	Val	Gln	Asp	Trp	Gly	His	His	Arg	Cys	Thr
1				5					10			

&lt;210&gt; 129

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; C3B ANTAGONIST

&lt;400&gt; 129

Cys	Val	Val	Gln	Asp	Trp	Gly	His	His	Ala	Cys
1				5					10	

&lt;210&gt; 130

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; MDM/HDM ANTAGONIST PEPTIDE

&lt;400&gt; 130

Thr	Phe	Ser	Asp	Leu	Trp
1				5	

&lt;210&gt; 131

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; MDM/HDM ANTAGONIST PEPTIDE

&lt;400&gt; 131

Gln	Glu	Thr	Phe	Ser	Asp	Leu	Trp	Lys	Leu	Leu	Pro
1				5					10		

&lt;210&gt; 132

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; MDM/HDM ANTAGONIST PEPTIDE

&lt;400&gt; 132

Gln	Pro	Thr	Phe	Ser	Asp	Leu	Trp	Lys	Leu	Leu	Pro
1				5					10		

&lt;210&gt; 133

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence



<220>  
 <223> MDM/HDM ANTAGONIST PEPTIDE  
 <400> 133  
 Gln Glu Thr Phe Ser Asp Tyr Trp Lys Leu Leu Pro  
 1 5 10

<210> 134  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> MDM/HDM ANTAGONIST PEPTIDE  
 <400> 134

Gln Pro Thr Phe Ser Asp Tyr Trp Lys Leu Leu Pro  
 1 5 10

<210> 135  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> MDM/HDM ANTAGONIST PEPTIDE  
 <400> 135

Met Pro Arg Phe Met Asp Tyr Trp Glu Gly Leu Asn  
 1 5 10

<210> 136  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> MDM/HDM ANTAGONIST PEPTIDE  
 <400> 136

Val Gln Asn Phe Ile Asp Tyr Trp Thr Gln Gln Phe  
 1 5 10

<210> 137  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> MDM/HDM ANTAGONIST PEPTIDE  
 <400> 137

Thr Gly Pro Ala Phe Thr His Tyr Trp Ala Thr Phe  
 1 5 10

<210> 138  
 <211> 15  
 <212> PRT

<213> Artificial Sequence

<220>

<223> MDM/HDM ANTAGONIST PEPTIDE

<400> 138 -

Ile	Asp	Arg	Ala	Pro	Thr	Phe	Arg	Asp	His	Trp	Phe	Ala	Leu	Val
1				5					10					15

<210> 139

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> MDM/HDM ANTAGONIST PEPTIDE

<400> 139

Pro	Arg	Pro	Ala	Leu	Val	Phe	Ala	Asp	Tyr	Trp	Glu	Thr	Leu	Tyr
1				5					10					15

<210> 140

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> MDM/HDM ANTAGONIST PEPTIDE

<400> 140

Pro	Ala	Phe	Ser	Arg	Phe	Trp	Ser	Asp	Leu	Ser	Ala	Gly	Ala	His
1				5					10					15

<210> 141

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> MDM/HDM ANTAGONIST PEPTIDE

<400> 141

Pro	Ala	Phe	Ser	Arg	Phe	Trp	Ser	Lys	Leu	Ser	Ala	Gly	Ala	His
1				5					10					15

<210> 142

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> MDM/HDM ANTAGONIST PEPTIDE

<220>

<221> misc\_feature

<222> (2, 4, 8 )..(9)

<223> Xaa = any amino acid

<400> 142

Pro Xaa Phe Xaa Asp Tyr Trp Xaa Xaa Leu  
 1 5 10

<210> 143  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> MDM/HDM ANTAGONIST PEPTIDE

<400> 143

Gln Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro  
 1 5 10

<210> 144  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> MDM/HDM ANTAGONIST PEPTIDE

<400> 144

Gln Pro Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro  
 1 5 10

<210> 145  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> MDM/HDM ANTAGONIST PEPTIDE

<400> 145

Gln Glu Thr Phe Ser Asp Tyr Trp Lys Leu Leu Pro  
 1 5 10

<210> 146  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> MDM/HDM ANTAGONIST PEPTIDE

<400> 146

Gln Pro Thr Phe Ser Asp Tyr Trp Lys Leu Leu Pro  
 1 5 10

<210> 147  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SELECTIN ANTAGONIST PEPTIDE

<400> 147

Asp Ile Thr Trp Asp Gln Leu Trp Asp Leu Met Lys  
1 5 10

<210> 148

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> SELECTIN ANTAGONIST PEPTIDE

<400> 148

Asp Ile Thr Trp Asp Glu Leu Trp Lys Ile Met Asn  
1 5 10

<210> 149

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> SELECTIN ANTAGONIST PEPTIDE

<400> 149

Asp Tyr Thr Trp Phe Glu Leu Trp Asp Met Met Gln  
1 5 10

<210> 150

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> SELECTIN ANTAGONIST PEPTIDE

<400> 150

Gln Ile Thr Trp Ala Gln Leu Trp Asn Met Met Lys  
1 5 10

<210> 151

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> SELECTIN ANTAGONIST PEPTIDE

<400> 151

Asp Met Thr Trp His Asp Leu Trp Thr Leu Met Ser  
1 5 10

<210> 152

<211> 12

<212> PRT

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; SELECTIN ANTAGONIST PEPTIDE

&lt;400&gt; 152

Asp Tyr Ser Trp His Asp Leu Trp Glu Met Met Ser  
 1 5 10

&lt;210&gt; 153

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; SELECTIN ANTAGONIST PEPTIDE

&lt;400&gt; 153

Glu Ile Thr Trp Asp Gln Leu Trp Glu Val Met Asn  
 1 5 10

&lt;210&gt; 154

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; SELECTIN ANTAGONIST PEPTIDE

&lt;400&gt; 154

His Val Ser Trp Glu Gln Leu Trp Asp Ile Met Asn  
 1 5 10

&lt;210&gt; 155

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; SELECTIN ANTAGONIST PEPTIDE

&lt;400&gt; 155

His Ile Thr Trp Asp Gln Leu Trp Arg Ile Met Thr  
 1 5 10

&lt;210&gt; 156

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; SELECTIN ANTAGONIST PEPTIDE

&lt;400&gt; 156

Arg Asn Met Ser Trp Leu Glu Leu Trp Glu His Met Lys  
 1 5 10

&lt;210&gt; 157

&lt;211&gt; 18

&lt;212&gt; PRT

<213> Artificial Sequence

<220>

<223> SELECTIN ANTAGONIST PEPTIDE

<400> 157 -

Ala Glu Trp Thr Trp Asp Gln Leu Trp His Val Met Asn Pro Ala Glu  
1 5 10 15

Ser Gln

<210> 158

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> SELECTIN ANTAGONIST PEPTIDE

<400> 158

His Arg Ala Glu Trp Leu Ala Leu Trp Glu Gln Met Ser Pro  
1 5 10

<210> 159

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> SELECTIN ANTAGONIST PEPTIDE

<400> 159

Lys Lys Glu Asp Trp Leu Ala Leu Trp Arg Ile Met Ser Val  
1 5 10

<210> 160

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> SELECTIN ANTAGONIST PEPTIDE

<400> 160

Ile Thr Trp Asp Gln Leu Trp Asp Leu Met Lys  
1 5 10

<210> 161

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> SELECTIN ANTAGONIST PEPTIDE

<400> 161

Asp Ile Thr Trp Asp Gln Leu Trp Asp Leu Met Lys

1 5

<210> 162  
<211> 12  
<212> PRT -  
<213> Artificial Sequence

<220>  
<223> SELECTIN ANTAGONIST PEPTIDE

<400> 162

Asp Ile Thr Trp Asp Gln Leu Trp Asp Leu Met Lys  
1 5 10

<210> 163  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SELECTIN ANTAGONIST PEPTIDE

<400> 163

Asp Ile Thr Trp Asp Gln Leu Trp Asp Leu Met Lys  
1 5 10

<210> 164  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> CALMODULIN ANTAGONIST PEPTIDE

<400> 164

Ser Cys Val Lys Trp Gly Lys Lys Glu Phe Cys G Ser  
1 5 10

<210> 165  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> CALMODULIN ANTAGONIST PEPTIDE

<400> 165

Ser Cys Trp Lys Tyr Trp Gly Lys Glu Cys Gly Ser  
1 5 10

<210> 166  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> CALMODULIN ANTAGONIST PEPTIDE

<400> 166

Ser Cys Tyr Glu Trp Gly Lys Leu Arg Trp Cys Gly Ser  
1 5 10

<210> 167 -  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> CALMODULIN ANTAGONIST PEPTIDE

<400> 167

Ser Cys Leu Arg Trp Gly Lys Trp Ser Asn Cys Gly Ser  
1 5 10

<210> 168  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> CALMODULIN ANTAGONIST PEPTIDE

<400> 168

Ser Cys Trp Arg Trp Gly Lys Tyr Gln Ile Cys Gly Ser  
1 5 10

<210> 169  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> CALMODULIN ANTAGONIST PEPTIDE

<400> 169

Ser Cys Val Ser Trp Gly Ala Leu Lys Leu Cys Gly Ser  
1 5 10

<210> 170  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> CALMODULIN ANTAGONIST PEPTIDE

<400> 170

Ser Cys Ile Arg Trp Gly Gln Asn Thr Phe Cys Gly Ser  
1 5 10

<210> 171  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> CALMODULIN ANTAGONIST PEPTIDE



<400> 171

Ser Cys Trp Gln Trp Gly Asn Leu Lys Ile Cys Gly Ser  
1 5 10

<210> 172

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> CALMODULIN ANTAGONIST PEPTIDE

<400> 172

Ser Cys Val Arg Trp Gly Gln Leu Ser Ile Cys Gly Ser  
1 5 10

<210> 173

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> CALMODULIN ANTAGONIST PEPTIDE

<400> 173

Leu Lys Lys Phe Asn Ala Arg Arg Lys Leu Lys Gly Ala Ile Leu Thr  
1 5 10 15

Thr Met Leu Ala Lys  
20

<210> 174

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> CALMODULIN ANTAGONIST PEPTIDE

<400> 174

Arg Arg Trp Lys Lys Asn Phe Ile Ala Val Ser Ala Ala Asn Arg Phe  
1 5 10 15

Lys Lys

<210> 175

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> CALMODULIN ANTAGONIST PEPTIDE

<400> 175

Arg Lys Trp Gln Lys Thr Gly His Ala Val Arg Ala Ile Gly Arg Leu  
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1 5 A-527.ST25.txt 15  
10

Ser Ser

<210> 176  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> CALMODULIN ANTAGONIST PEPTIDE

<400> 176

Ile Asn Leu Lys Ala Leu Ala Ala Leu Ala Lys Lys Ile Leu  
1 5 10

<210> 177  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> CALMODULIN ANTAGONIST PEPTIDE

<400> 177

Lys Ile Trp Ser Ile Leu Ala Pro Leu Gly Thr Thr Leu Val Lys Leu  
1 5 10 15

Val Ala

<210> 178  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> CALMODULIN ANTAGONIST PEPTIDE

<400> 178

Leu Lys Lys Leu Leu Lys Leu Leu Lys Lys Leu Leu Lys Leu  
1 5 10

<210> 179  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> CALMODULIN ANTAGONIST PEPTIDE

<400> 179

Leu Lys Trp Lys Lys Leu Leu Lys Leu Leu Lys Lys Leu Leu Lys Lys  
1 5 10 15

Leu Leu

<210> 180  
 <211> 17  
 <212> PRT -  
 <213> Artificial Sequence

<220>  
 <223> CALMODULIN ANTAGONIST PEPTIDE

<400> 180

Ala Glu Trp Pro Ser Leu Thr Glu Ile Lys Thr Leu Ser His Phe Ser  
 1 5 10 15

Val

<210> 181  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> CALMODULIN ANTAGONIST PEPTIDE

<400> 181

Ala Glu Trp Pro Ser Pro Thr Arg Val Ile Ser Thr Thr Tyr Phe Gly  
 1 5 10 15

Ser

<210> 182  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> CALMODULIN ANTAGONIST PEPTIDE

<400> 182

Ala Glu Leu Ala His Trp Pro Pro Val Lys Thr Val Leu Arg Ser Phe  
 1 5 10 15

Thr

<210> 183  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> CALMODULIN ANTAGONIST PEPTIDE

<400> 183

Ala Glu Gly Ser Trp Leu Gln Leu Leu Asn Leu Met Lys Gln Met Asn  
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1 5 A-527.ST25.txt 15  
10

Asn

<210> 184  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> CALMODULIN ANTAGONIST PEPTIDE

<400> 184

Ala Glu Trp Pro Ser Leu Thr Glu Ile Lys  
1 5 10

<210> 185  
<211> 27  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> VINCULIN-BINDING

<400> 185

Ser Thr Gly Gly Phe Asp Asp Val Tyr Asp Trp Ala Arg Gly Val Ser  
1 5 10 15

Ser Ala Leu Thr Thr Thr Leu Val Ala Thr Arg  
20 25

<210> 186  
<211> 27  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> VINCULIN-BINDING

<400> 186

Ser Thr Gly Gly Phe Asp Asp Val Tyr Asp Trp Ala Arg Arg Val Ser  
1 5 10 15

Ser Ala Leu Thr Thr Thr Leu Val Ala Thr Arg  
20 25

<210> 187  
<211> 30  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> VINCULIN-BINDING

<400> 187

Ser Arg Gly Val Asn Phe Ser Glu Trp Leu Tyr Asp Met Ser Ala Ala  
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1                      5                      10                      15

Met Lys Glu Ala Ser Asn Val Phe Pro Ser Arg Arg Ser Arg  
                     20                      25                      30

<210> 188  
 <211> 30  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> VINCULIN-BINDING

<400> 188

Ser Ser Gln Asn Trp Asp Met Glu Ala Gly Val Glu Asp Leu Thr Ala  
 1                      5                      10                      15

Ala Met Leu Gly Leu Leu Ser Thr Ile His Ser Ser Ser Arg  
                     20                      25                      30

<210> 189  
 <211> 31  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> VINCULIN-BINDING

<400> 189

Ser Ser Pro Ser Leu Tyr Thr Gln Phe Leu Val Asn Tyr Glu Ser Ala  
 1                      5                      10                      15

Ala Thr Arg Ile Gln Asp Leu Leu Ile Ala Ser Arg Pro Ser Arg  
                     20                      25                      30

<210> 190  
 <211> 31  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> VINCULIN-BINDING

<400> 190

Ser Ser Thr Gly Trp Val Asp Leu Leu Gly Ala Leu Gln Arg Ala Ala  
 1                      5                      10                      15

Asp Ala Thr Arg Thr Ser Ile Pro Pro Ser Leu Gln Asn Ser Arg  
                     20                      25                      30

<210> 191  
 <211> 18  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> VINCULIN-BINDING

<400> 191

Asp Val Tyr Thr Lys Lys Glu Leu Ile Glu Cys Ala Arg Arg Val Ser  
1 5 10 15

Glu Lys

<210> 192

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> C4BP-BINDING

<400> 192

Glu Lys Gly Ser Tyr Tyr Pro Gly Ser Gly Ile Ala Gln Phe His Ile  
1 5 10 15

Asp Tyr Asn Asn Val Ser  
20

<210> 193

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> C4BP-BINDING

<400> 193

Ser Gly Ile Ala Gln Phe His Ile Asp Tyr Asn Asn Val Ser Ser Ala  
1 5 10 15

Glu Gly Trp His Val Asn  
20

<210> 194

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> C4BP-BINDING

<400> 194

Leu Val Thr Val Glu Lys Gly Ser Tyr Tyr Pro Gly Ser Gly Ile Ala  
1 5 10 15

Gln Phe His Ile Asp Tyr Asn Asn Val Ser Ser Ala Glu Gly Trp His  
20 25 30

Val Asn

<210> 195  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> C4BP-BINDING

<400> 195

Ser Gly Ile Ala Gln Phe His Ile Asp Tyr Asn Asn Val Ser  
 1 5 10

<210> 196  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> UKR ANTAGONIST PEPTIDE

<400> 196

Ala Glu Pro Met Pro His Ser Leu Asn Phe Ser Gln Tyr Leu Trp Tyr  
 1 5 10 15

Thr

<210> 197  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> UKR ANTAGONIST PEPTIDE

<400> 197

Ala Glu His Thr Tyr Ser Ser Leu Trp Asp Thr Tyr Ser Pro Leu Ala  
 1 5 10 15

Phe

<210> 198  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> UKR ANTAGONIST PEPTIDE

<400> 198

Ala Glu Leu Asp Leu Trp Met Arg His Tyr Pro Leu Ser Phe Ser Asn  
 1 5 10 15

Arg

<210> 199  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> UKR ANTAGONIST PEPTIDE

<400> 199

Ala Glu Ser Ser Leu Trp Thr Arg Tyr Ala Trp Pro Ser Met Pro Ser  
 1 5 10 15

Tyr

<210> 200  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> UKR ANTAGONIST PEPTIDE

<400> 200

Ala Glu Trp His Pro Gly Leu Ser Phe Gly Ser Tyr Leu Trp Ser Lys  
 1 5 10 15

Thr

<210> 201  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> UKR ANTAGONIST PEPTIDE

<400> 201

Ala Glu Pro Ala Leu Leu Asn Trp Ser Phe Phe Phe Asn Pro Gly Leu  
 1 5 10 15

His

<210> 202  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> UKR ANTAGONIST PEPTIDE

<400> 202

Ala Glu Trp Ser Phe Tyr Asn Leu His Leu Pro Glu Pro Gln Thr Ile  
 1 5 10 15



Phe

<210> 203 -  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> UKR ANTAGONIST PEPTIDE

<400> 203

Ala Glu Pro Leu Asp Leu Trp Ser Leu Tyr Ser Leu Pro Pro Leu Ala  
 1 5 10 15

Met

<210> 204  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> UKR ANTAGONIST PEPTIDE

<400> 204

Ala Glu Pro Thr Leu Trp Gln Leu Tyr Gln Phe Pro Leu Arg Leu Ser  
 1 5 10 15

Gly

<210> 205  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> UKR ANTAGONIST PEPTIDE

<400> 205

Ala Glu Ile Ser Phe Ser Glu Leu Met Trp Leu Arg Ser Thr Pro Ala  
 1 5 10 15

Phe

<210> 206  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> UKR ANTAGONIST PEPTIDE

<400> 206

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Ala Glu Leu Ser Glu Ala Asp Leu Trp Thr Thr Trp Phe Gly Met Gly  
1 5 10 15

Ser -

<210> 207  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> UKR ANTAGONIST PEPTIDE

<400> 207

Ala Glu Ser Ser Leu Trp Arg Ile Phe Ser Pro Ser Ala Leu Met Met  
1 5 10 15

Ser

<210> 208  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> UKR ANTAGONIST PEPTIDE

<400> 208

Ala Glu Ser Leu Pro Thr Leu Thr Ser Ile Leu Trp Gly Lys Glu Ser  
1 5 10 15

Val

<210> 209  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> UKR ANTAGONIST PEPTIDE

<400> 209

Ala Glu Thr Leu Phe Met Asp Leu Trp His Asp Lys His Ile Leu Leu  
1 5 10 15

Thr

<210> 210  
<211> 17  
<212> PRT  
<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; UKR ANTAGONIST PEPTIDE

&lt;400&gt; 210

Ala Glu Ile Leu Asn Phe Pro Leu Trp His Glu Pro Leu Trp Ser Thr  
 1                   5                   10                   15

Glu

&lt;210&gt; 211

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; UKR ANTAGONIST PEPTIDE

&lt;400&gt; 211

Ala Glu Ser Gln Thr Gly Thr Leu Asn Thr Leu Phe Trp Asn Thr Leu  
 1                   5                   10                   15

Arg

&lt;210&gt; 212

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; IL-1 ANTAGONIST PEPTIDE

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1)

&lt;223&gt; Xaa is V, L, I, E, P, G, Y, M, T or D.

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (2)..(2)

&lt;223&gt; Xaa is Y, W or F.

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (3)..(3)

&lt;223&gt; Xaa is F, W or Y.

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (5)..(5)

&lt;223&gt; Xaa is P or Azetidine.

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (7)..(7)

&lt;223&gt; Xaa is S, A, V or L.

<220>  
 <221> misc\_feature  
 <222> (8)..(8)  
 <223> Xaa is V, L, I or E.

<220>  
 <221> misc\_feature  
 <222> (9)..(9)  
 <223> Xaa is Q or P.

<400> 212

Xaa Xaa Xaa Gln Xaa Tyr Xaa Xaa Xaa  
 1 5

<210> 213  
 <211> 21  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<400> 213

Thr Ala Asn Val Ser Ser Phe Glu Trp Thr Pro Tyr Tyr Trp Gln Pro .  
 1 5 10 15

Tyr Ala Leu Pro Leu  
 20

<210> 214  
 <211> 18  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE  
 <400> 214

Ser Trp Thr Asp Tyr Gly Tyr Trp Gln Pro Tyr Ala Leu Pro Ile Ser  
 1 5 10 15

Gly Leu

<210> 215  
 <211> 21  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE  
 <400> 215

Glu Thr Pro Phe Thr Trp Glu Glu Ser Asn Ala Tyr Tyr Trp Gln Pro  
 1 5 10 15

Tyr Ala Leu Pro Leu  
 20

<210> 216  
 <211> 21  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<400> 216

Glu Asn Thr Tyr Ser Pro Asn Trp Ala Asp Ser Met Tyr Trp Gln Pro  
 1 5 10 15

Tyr Ala Leu Pro Leu  
 20

<210> 217  
 <211> 21  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<400> 217

Ser Val Gly Glu Asp His Asn Phe Trp Thr Ser Glu Tyr Trp Gln Pro  
 1 5 10 15

Tyr Ala Leu Pro Leu  
 20

<210> 218  
 <211> 21  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<400> 218

Asp Gly Tyr Asp Arg Trp Arg Gln Ser Gly Glu Arg Tyr Trp Gln Pro  
 1 5 10 15

Tyr Ala Leu Pro Leu  
 20

<210> 219  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<400> 219

Phe Glu Trp Thr Pro Gly Tyr Trp Gln Pro Tyr  
 1 5 10

<210> 220  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE  
 <400> 220

Phe Glu Trp Thr Pro Gly Tyr Trp Gln His Tyr  
 1 5 10

<210> 221  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa = azetidine

<400> 221

Phe Glu Trp Thr Pro Gly Trp Tyr Gln Xaa Tyr  
 1 5 10

<210> 222  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (1)..(1)  
 <223> Position 1, optionally acetlated at N terminus

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa = azetidine

<400> 222

Phe Glu Trp Thr Pro Gly Trp Tyr Gln Xaa Tyr  
 1 5 10

<210> 223  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> IL-1 ANTAGONIST PEPTIDE

<220>

<221> misc\_feature

<222> (11)..(11)

<223> Position 11, Xaa = azetidine

<400> 223

Phe	Glu	Trp	Thr	Pro	Gly	Trp	Pro	Tyr	Gln	Xaa	Tyr
1				5					10		

<210> 224

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-1 ANTAGONIST PEPTIDE

<220>

<221> misc\_feature

<222> (10)..(10)

<223> Position 10, Xaa = azetidine

<400> 224

Phe	Ala	Trp	Thr	Pro	Gly	Tyr	Trp	Gln	Xaa	Tyr
1				5					10	

<210> 225

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-1 ANTAGONIST PEPTIDE

<220>

<221> misc\_feature

<222> (10)..(10)

<223> Position 10, Xaa = azetidine

<400> 225

Phe	Glu	Trp	Ala	Pro	Gly	Tyr	Trp	Gln	Xaa	Tyr
1				5					10	

<210> 226

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-1 ANTAGONIST PEPTIDE

<220>

<221> misc\_feature

<222> (10)..(10)

<223> Position 10, Xaa = azetidine

&lt;400&gt; 226

Phe Glu Trp Val Pro Gly Tyr Trp Gln Xaa Tyr  
 1 5 10

&lt;210&gt; 227

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; IL-1 ANTAGONIST PEPTIDE

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (10)..(10)

&lt;223&gt; Position 10, Xaa = azetidine

&lt;400&gt; 227

Phe Glu Trp Thr Pro Gly Tyr Trp Gln Xaa Tyr  
 1 5 10

&lt;210&gt; 228

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; IL-1 ANTAGONIST PEPTIDE

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1)

&lt;223&gt; Position 1, optionally acetylated at N terminus

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (10)..(10)

&lt;223&gt; Position 10, Xaa = azetidine

&lt;400&gt; 228

Phe Glu Trp Thr Pro Gly Tyr Trp Gln Xaa Tyr  
 1 5 10

&lt;210&gt; 229

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; IL-1 ANTAGONIST PEPTIDE

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (6 )..(6)

&lt;223&gt; Position 6, Xaa products = "MeGly"

&lt;220&gt;



<221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa = azetidine

<400> 229 -

Phe Glu Trp Thr Pro Xaa Trp Tyr Gln Xaa Tyr  
 1 5 10

<210> 230  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (6)..(6)  
 <223> Position 6, Xaa = MeGly

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa = azetidine

<400> 230

Phe Glu Trp Thr Pro Xaa Trp Tyr Gln Xaa Tyr  
 1 5 10

<210> 231  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<400> 231

Phe Glu Trp Thr Pro Gly Tyr Tyr Gln Pro Tyr  
 1 5 10

<210> 232  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<400> 232

Phe Glu Trp Thr Pro Gly Trp Trp Gln Pro Tyr  
 1 5 10

<210> 233  
 <211> 11  
 <212> PRT

<213> Artificial Sequence

<220>

<223> IL-1 ANTAGONIST PEPTIDE

<400> 233 -

Phe Glu Trp Thr Pro Asn Tyr Trp Gln Pro Tyr  
1 5 10

<210> 234

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-1 ANTAGONIST PEPTIDE

<220>

<221> misc\_feature

<222> (5)..(5)

<223> Position 5, Xaa = pipecolic acid

<220>

<221> misc\_feature

<222> (10)..(10)

<223> Position 10, Xaa = azetidine

<400> 234

Phe Glu Trp Thr Xaa Val Tyr Trp Gln Xaa Tyr  
1 5 10

<210> 235

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-1 ANTAGONIST PEPTIDE

<220>

<221> misc\_feature

<222> (5)..(5)

<223> Position 5, Xaa = pipecolic acid

<220>

<221> misc\_feature

<222> (10)..(10)

<223> Position 10, Xaa = azetidine

<400> 235

Phe Glu Trp Thr Xaa Gly Tyr Trp Gln Xaa Tyr  
1 5 10

<210> 236

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-1 ANTAGONIST PEPTIDE

<220>

<221> misc\_feature

<222> (6 )..(6)

<223> Position 6, Xaa = Aib

<220>

<221> misc\_feature

<222> (10)..(10)

<223> Position 10, Xaa = azetidine

<400> 236

Phe Glu Trp Thr Pro Xaa Tyr Trp Gln Xaa Tyr  
1 5 10

<210> 237

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-1 ANTAGONIST PEPTIDE

<220>

<221> misc\_feature

<222> (5 )..(5)

<223> Position 5, Xaa = MeGly

<220>

<221> misc\_feature

<222> (10)..(10)

<223> Position 10, Xaa = azetidine

<400> 237

Phe Glu Trp Thr Xaa Gly Tyr Trp Gln Xaa Tyr  
1 5 10

<210> 238

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-1 ANTAGONIST PEPTIDE

<220>

<221> misc\_feature

<222> (11)..(11)

<223> Position 11, amino group added at C terminus

<400> 238

Phe Glu Trp Thr Pro Gly Tyr Trp Gln Pro Tyr  
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1 5

<210> 239  
<211> 11  
<212> PRT -  
<213> Artificial Sequence  
  
<220>  
<223> IL-1 ANTAGONIST PEPTIDE  
  
<220>  
<221> misc\_feature  
<222> (11)..(11)  
<223> Position 11, amino group added at C-terminus

<400> 239

Phe Glu Trp Thr Pro Gly Tyr Trp Gln His Tyr  
1 5 10

<210> 240  
<211> 11  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> IL-1 ANTAGONIST PEPTIDE  
  
<220>  
<221> misc\_feature  
<222> (10)..(10)  
<223> Position 10, Xaa is an azetidine residue  
Position 11 amino group added at C-terminus

<220>  
<221> misc\_feature  
<222> (11)..(11)  
<223> Position 11 amino group added at C-terminus

<400> 240

Phe Glu Trp Thr Pro Gly Trp Tyr Gln Xaa Tyr  
1 5 10

<210> 241  
<211> 11  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> IL-1 ANTAGONIST PEPTIDE  
  
<220>  
<221> misc\_feature  
<222> (1)..(1)  
<223> Position 1 optionally acetylated at N-terminus

<220>  
<221> misc\_feature  
<222> (10)..(10)  
<223> Position 10, Xaa is an azetidine residue

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> Position 11 amino group added at C-terminus

<400> 241

Phe	Glu	Trp	Thr	Pro	Gly	Trp	Tyr	Gln	Xaa	Tyr
1				5					10	

<210> 242  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (8)..(8)  
 <223> Position 8, Xaa is a phyosphotyrosyl residue

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa is an azetidine residue

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> Position 11 amino group added at C-terminus

<400> 242

Phe	Glu	Trp	Thr	Pro	Gly	Trp	Xaa	Gln	Xaa	Tyr
1				5					10	

<210> 243  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa is an azetidine residue

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> Position 11 amino group added at C-terminus

<400> 243

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Phe Ala Trp Thr Pro Gly Tyr Trp Gln Xaa Tyr  
 1                   5                   10

<210> 244  
 <211> 11 -  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa is an azetidine residue

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> Position 11 amino group added at C-terminus

<400> 244

Phe Glu Trp Ala Pro Gly Tyr Trp Gln Xaa Tyr  
 1                   5                   10

<210> 245  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa is an azetidine residue

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> Position 11 amino group added at C-terminus

<400> 245

Phe Glu Trp Val Pro Gly Tyr Trp Gln Xaa Tyr  
 1                   5                   10

<210> 246  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa is an azetidine residue

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> Position 11 amino group added at C-terminus

<400> 246

Phe	Glu	Trp	Thr	Pro	Gly	Tyr	Trp	Gln	Xaa	Tyr
1				5					10	

<210> 247  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (1)..(1)  
 <223> Position 1 acetylated at N-terminus

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa is an azetidine residue

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> Position 11 amino group added at C-terminus

<400> 247

Phe	Glu	Trp	Thr	Pro	Gly	Tyr	Trp	Gln	Xaa	Tyr
1				5					10	

<210> 248  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (6)..(6)  
 <223> Position 6, D amino acid residue

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa is an azetidine residue

<220>  
 <221> misc\_feature

<222> (11)..(11)  
 <223> Position 11 amino group added at C-terminus

<400> 248

Phe Glu Trp Thr Pro Ala Trp Tyr Gln Xaa Tyr  
 1 5 10

<210> 249  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (6)..(6)  
 <223> Position 6, Xaa is a sarcosine residue

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa is an azetidine residue

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> Position 11 amino group added at C-terminus

<400> 249

Phe Glu Trp Thr Pro Xaa Trp Tyr Gln Xaa Tyr  
 1 5 10

<210> 250  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> Position 11 amino group added at C-terminus

<400> 250

Phe Glu Trp Thr Pro Gly Tyr Tyr Gln Pro Tyr  
 1 5 10

<210> 251  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>



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 <223> IL-1 ANTAGONIST PEPTIDE  
 <220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> Position 11 amino group added at C-terminus

<400> 251

Phe Glu Trp Thr Pro Gly Trp Trp Gln Pro Tyr  
 1 5 10

<210> 252  
 <211> 11  
 <212> PRT  
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<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> Position 11 amino group added at C-terminus

<400> 252

Phe Glu Trp Thr Pro Asn Tyr Trp Gln Pro Tyr  
 1 5 10

<210> 253  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (6)..(6)  
 <223> Position 6, D amino acid residue

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa is an azetidine residue

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> Position 11 amino group added at C-terminus

<400> 253

Phe Glu Trp Thr Pro Val Tyr Trp Gln Xaa Tyr  
 1 5 10

<210> 254  
 <211> 11

<212> PRT  
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 <220>  
 <223> IL-1 ANTAGONIST PEPTIDE  
 <220>  
 <221> misc\_feature  
 <222> (5)..(5)  
 <223> Position 5, Xaa is a pipecolic acid residue

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa is an azetidine residue

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> Position 11 amino group added at C-terminus

<400> 254

Phe Glu Trp Thr Xaa Gly Tyr Trp Gln Xaa Tyr  
 1 5 10

<210> 255  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (6)..(6)  
 <223> Position 6, Xaa = pipecolic acid

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa = azetidine

<400> 255

Phe Glu Trp Thr Pro Xaa Tyr Trp Gln Xaa Tyr  
 1 5 10

<210> 256  
 <211> 11  
 <212> PRT  
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<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (5)..(5)  
 <223> Position 5, Xaa = MeGly

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa = azetidine

<400> 256

Phe Glu Trp Thr Xaa Gly Tyr Trp Gln Xaa Tyr  
 1 5 10

<210> 257  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<400> 257

Phe Glu Trp Thr Pro Gly Tyr Trp Gln Pro Tyr Ala Leu Pro Leu  
 1 5 10 15

<210> 258  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (1)..(1)  
 <223> Position 1, Xaa is a 1-naphthylalanine residue

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa is an azetidine residue

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> Position 11 amino group added at C-terminus

<400> 258

Xaa Glu Trp Thr Pro Gly Tyr Tyr Gln Xaa Tyr  
 1 5 10

<210> 259  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa is an azetidine residue  
  
 <220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> Position 11 amino group added at C-terminus  
  
 <400> 259

Tyr Glu Trp Thr Pro Gly Tyr Tyr Gln Xaa Tyr  
 1                      5                      10

<210> 260  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa is an azetidine residue

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> Position 11 amino group added at C-terminus

<400> 260

Phe Glu Trp Val Pro Gly Tyr Tyr Gln Xaa Tyr  
 1                      5                      10

<210> 261  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (6)..(6)  
 <223> Position 6, D amino acid residue

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa is an azetidine residue

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> Position 11 amino group added at C-terminus

<400> 261

Phe Glu Trp Thr Pro Ser Tyr Tyr Gln Xaa Tyr  
 1 5 10

<210> 262 -  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (6)..(6)  
 <223> Position 6, D amino acid residue

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa is an azetidine residue

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> Position 11 amino group added at C-terminus

<400> 262

Phe Glu Trp Thr Pro Asn Tyr Tyr Gln Xaa Tyr  
 1 5 10

<210> 263  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<400> 263

Thr Lys Pro Arg  
 1

<210> 264  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<400> 264

Arg Lys Ser Ser Lys  
 1 5

<210> 265  
 <211> 5  
 <212> PRT

<213> Artificial Sequence

<220>

<223> IL-1 ANTAGONIST PEPTIDE

<400> 265 -

Arg Lys Gln Asp Lys

1

5

<210> 266

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-1 ANTAGONIST PEPTIDE

<400> 266

Asn Arg Lys Gln Asp Lys

1

5

<210> 267

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-1 ANTAGONIST PEPTIDE

<400> 267

Arg Lys Gln Asp Lys Arg

1

5

<210> 268

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-1 ANTAGONIST PEPTIDE

<400> 268

Glu Asn Arg Lys Gln Asp Lys Arg Phe

1

5

<210> 269

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-1 ANTAGONIST PEPTIDE

<400> 269

Val Thr Lys Phe Tyr Phe

1

5

<210> 270

<211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<400> 270

Val Thr Lys Phe Tyr  
 1 5

<210> 271  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IL-1 ANTAGONIST PEPTIDE

<400> 271

Val Thr Asp Phe Tyr  
 1 5

<210> 272  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> MAST CELL ANTAGONISTS/ PROTEASE INHIBITOR PEPTIDE

<400> 272

Ser Gly Ser Gly Val Leu Lys Arg Pro Leu Pro Ile Leu Pro Val Thr  
 1 5 10 15

Arg

<210> 273  
 <211> 17  
 <212> PRT  
 <213> Artificial SEquence

<220>  
 <223> MAST CELL ANTAGONISTS/ PROTEASE INHIBITOR PEPTIDE

<400> 273

Arg Trp Leu Ser Ser Arg Pro Leu Pro Pro Leu Pro Leu Pro Pro Arg  
 1 5 10 15

Thr

<210> 274  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> MAST CELL ANTAGONISTS/ PROTEASE INHIBITOR PEPTIDE

<400> 274

Gly Ser Gly Ser Tyr Asp Thr Leu Ala Leu Pro Ser Leu Pro Leu His  
1 5 10 15

Pro Met Ser Ser  
20

<210> 275

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> MAST CELL ANTAGONISTS/ PROTEASE INHIBITOR PEPTIDE

<400> 275

Gly Ser Gly Ser Tyr Asp Thr Arg Ala Leu Pro Ser Leu Pro Leu His  
1 5 10 15

Pro Met Ser Ser  
20

<210> 276

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> MAST CELL ANTAGONISTS/ PROTEASE INHIBITOR PEPTIDE

<400> 276

Gly Ser Gly Ser Ser Gly Val Thr Met Tyr Pro Lys Leu Pro Pro His  
1 5 10 15

Trp Ser Met Ala  
20

<210> 277

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> MAST CELL ANTAGONISTS/ PROTEASE INHIBITOR PEPTIDE

<400> 277

Gly Ser Gly Ser Ser Gly Val Arg Met Tyr Pro Lys Leu Pro Pro His  
1 5 10 15

Trp Ser Met Ala  
20

<210> 278



<211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> MAST CELL ANTAGONISTS/ PROTEASE INHIBITOR PEPTIDE

<400> 278

Gly Ser Gly Ser Ser Ser Met Arg Met Val Pro Thr Ile Pro Gly Ser  
 1 5 10 15

Ala Lys His Gly  
 20

<210> 279  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ANTI-HBV

<400> 279

Leu Leu Gly Arg Met Lys  
 1 5

<210> 280  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ANTI-HBV

<400> 280

Ala Leu Leu Gly Arg Met Lys Gly  
 1 5

<210> 281  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ANTI-HBV

<400> 281

Leu Asp Pro Ala Phe Arg  
 1 5

<210> 282  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SH3 ANTAGONIST PEPTIDE

<400> 282

Arg Pro Leu Pro Pro Leu Pro  
1 5

<210> 283 -  
<211> 7  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> SH3 ANTAGONIST PEPTIDE  
  
<400> 283

Arg Glu Leu Pro Pro Leu Pro  
1 5

<210> 284  
<211> 7  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> SH3 ANTAGONIST PEPTIDE  
  
<400> 284

Ser Pro Leu Pro Pro Leu Pro  
1 5

<210> 285  
<211> 7  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> SH3 ANTAGONIST PEPTIDE  
  
<400> 285

Gly Pro Leu Pro Pro Leu Pro  
1 5

<210> 286  
<211> 7  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> SH3 ANTAGONIST PEPTIDE  
  
<400> 286

Arg Pro Leu Pro Ile Pro Pro  
1 5

<210> 287  
<211> 7  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> SH3 ANTAGONIST PEPTIDE

<400> 287

Arg Pro Leu Pro Ile Pro Pro  
1 5

<210> 288

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> SH3 ANTAGONIST PEPTIDE

<400> 288

Arg Arg Leu Pro Pro Thr Pro  
1 5

<210> 289

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> SH3 ANTAGONIST PEPTIDE

<400> 289

Arg Gln Leu Pro Pro Thr Pro  
1 5

<210> 290

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> SH3 ANTAGONIST PEPTIDE

<400> 290

Arg Pro Leu Pro Ser Arg Pro  
1 5

<210> 291

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> SH3 ANTAGONIST PEPTIDE

<400> 291

Arg Pro Leu Pro Thr Arg Pro  
1 5

<210> 292

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> SH3 ANTAGONIST PEPTIDE

<400> 292

Ser Arg Leu Pro Pro Leu Pro  
1 5

<210> 293

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> SH3 ANTAGONIST PEPTIDE

<400> 293

Arg Ala Leu Pro Ser Pro Pro  
1 5

<210> 294

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> SH3 ANTAGONIST PEPTIDE

<400> 294

Arg Arg Leu Pro Arg Thr Pro  
1 5

<210> 295

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> SH3 ANTAGONIST PEPTIDE

<400> 295

Arg Pro Val Pro Pro Ile Thr  
1 5

<210> 296

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> SH3 ANTAGONIST PEPTIDE

<400> 296

Ile Leu Ala Pro Pro Val Pro  
1 5

<210> 297

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> SH3 ANTAGONIST PEPTIDE

<400> 297 -

Arg Pro Leu Pro Met Leu Pro  
1 5

<210> 298

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> SH3 ANTAGONIST PEPTIDE

<400> 298

Arg Pro Leu Pro Ile Leu Pro  
1 5

<210> 299

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> SH3 ANTAGONIST PEPTIDE

<400> 299

Arg Pro Leu Pro Ser Leu Pro  
1 5

<210> 300

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> SH3 ANTAGONIST PEPTIDE

<400> 300

Arg Pro Leu Pro Ser Leu Pro  
1 5

<210> 301

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> SH3 ANTAGONIST PEPTIDE

<400> 301

Arg Pro Leu Pro Met Ile Pro  
1 5

<210> 302

<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SH3 ANTAGONIST PEPTIDE

<400> 302

Arg Pro Leu Pro Leu Ile Pro  
1 5

<210> 303  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SH3 ANTAGONIST PEPTIDE

<400> 303

Arg Pro Leu Pro Pro Thr Pro  
1 5

<210> 304  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SH3 ANTAGONIST PEPTIDE

<400> 304

Arg Ser Leu Pro Pro Leu Pro  
1 5

<210> 305  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SH3 ANTAGONIST PEPTIDE

<400> 305

Arg Pro Gln Pro Pro Pro Pro  
1 5

<210> 306  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SH3 ANTAGONIST PEPTIDE

<400> 306

Arg Gln Leu Pro Ile Pro Pro  
1 5

<210> 307  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SH3 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (1, 2, 3)..(11)  
 <223> Xaa = any amino acid

<400> 307

Xaa Xaa Xaa Arg Pro Leu Pro Pro Leu Pro Xaa Pro  
 1 5 10

<210> 308  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SH3 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (1, 2, 3, 11)..(12)  
 <223> Xaa = any amino acid

<400> 308

Xaa Xaa Xaa Arg Pro Leu Pro Pro Ile Pro Xaa Xaa  
 1 5 10

<210> 309  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SH3 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (1, 2, 3, 11)..(12)  
 <223> Xaa = any amino acid

<400> 309

Xaa Xaa Xaa Arg Pro Leu Pro Pro Leu Pro Xaa Xaa  
 1 5 10

<210> 310  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SH3 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (2, 3, 10)..(11)  
 <223> Xaa = any amino acid

<400> 310

Arg Xaa Xaa Arg Pro Leu Pro Pro Leu Pro Xaa Pro  
 1 5 10

<210> 311  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SH3 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (2)..(3)  
 <223> Xaa = any amino acid

<400> 311

Arg Xaa Xaa Arg Pro Leu Pro Pro Leu Pro Pro Pro  
 1 5 10

<210> 312  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SH3 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (11)..(12)  
 <223> Xaa = any amino acid

<400> 312

Pro Pro Pro Tyr Pro Pro Pro Pro Ile Pro Xaa Xaa  
 1 5 10

<210> 313  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SH3 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (11)..(12)  
 <223> Xaa = any amino acid

<400> 313



Pro Pro Pro Tyr Pro Pro Pro Pro Val Pro Xaa Xaa  
1 5 10

<210> 314 -  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SH3 ANTAGONIST PEPTIDE

<220>  
<221> misc\_feature  
<222> (2, 3)..(8)  
<223> Xaa (Pos2, 3, 8) is any amino acid

<220>  
<221> misc\_feature  
<222> (9)..(9)  
<223> Xaa (Pos 9) represents an aliphatic amino acid residue

<400> 314

Leu Xaa Xaa Arg Pro Leu Pro Xaa Xaa Pro  
1 5 10

<210> 315  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SH3 ANTAGONIST PEPTIDE

<220>  
<221> misc\_feature  
<222> (1)..(1)  
<223> Position 1, Xaa is an aliphatic amino acid residue

<220>  
<221> misc\_feature  
<222> (2, 3)..(8)  
<223> Positions 2, 3 & 8, Xaa is any amino acid

<400> 315

Xaa Xaa Xaa Arg Pro Leu Pro Xaa Leu Pro  
1 5 10

<210> 316  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> SH3 ANTAGONIST PEPTIDE

<220>  
<221> misc\_feature

<222> (3)..(3)  
 <223> Position 3, Xaa is any amino acid residue

<220> -  
 <221> misc\_feature  
 <222> (4)..(4)  
 <223> Position 4, Xaa is an aromatic amino acid residue

<220>  
 <221> misc\_feature  
 <222> (9)..(9)  
 <223> Position 9, Xaa is an aliphatic amino acid residue

<400> 316

Pro Pro Xaa Xaa Tyr Pro Pro Pro Xaa Pro  
 1 5 10

<210> 317  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SH3 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (1)..(1)  
 <223> Position 1, Xaa is a basic amino acid residue

<220>  
 <221> misc\_feature  
 <222> (4)..(4)  
 <223> Position 4, Xaa is an aliphatic amino acid residue

<220>  
 <221> misc\_feature  
 <222> (6)..(9)  
 <223> Positions 6 & 9, Xaa is any amino acid residue

<400> 317

Xaa Pro Pro Xaa Pro Xaa Lys Pro Xaa Trp Leu  
 1 5 10

<210> 318  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SH3 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (3, 4)..(6)  
 <223> Positions 3, 4 & 6, Xaa is an aliphatic amino acid residue

<220>  
 <221> misc\_feature  
 <222> (8)..(8)  
 <223> Position 8, Xaa is a basic amino acid residue

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Position 10, Xaa is any amino acid residue

<400> 318

Arg Pro Xaa Xaa Pro Xaa Arg Xaa Ser Xaa Pro  
 1 5 10

<210> 319  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SH3 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (8)..(9)  
 <223> Xaa = any amino acid

<400> 319

Pro Pro Val Pro Pro Arg Pro Xaa Xaa Thr Leu  
 1 5 10

<210> 320  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SH3 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (1, 3)..(6)  
 <223> Positions 1, 3 and 6, Xaa is an aliphatic amino acid residue

<400> 320

Xaa Pro Xaa Leu Pro Xaa Lys  
 1 5

<210> 321  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SH3 ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (1)..(1)  
 <223> Position 1, Xaa is a basic amino acid residue  
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<220>  
 <221> misc\_feature  
 <222> (2)..(2)  
 <223> Position 2, Xaa is an aromatic amino acid residue

<220>  
 <221> misc\_feature  
 <222> (4)..(8)  
 <223> Positions 4 & 8, Xaa is any amino acid residue

<400> 321

Xaa Xaa Asp Xaa Pro Leu Pro Xaa Leu Pro  
 1 5 10

<210> 322  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> INHIBITION OF PLATELET AGGREGATION

<220>  
 <221> misc\_feature  
 <222> (2)..(3)  
 <223> Xaa = any amino acid

<400> 322

Cys Xaa Xaa Arg Gly Asp Cys  
 1 5

<210> 323  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SRC ANTAGONIST

<400> 323

Arg Pro Leu Pro Pro Leu Pro  
 1 5

<210> 324  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SRC ANTAGONIST

&lt;400&gt; 324

Pro Pro Val Pro Pro Arg  
1 5

&lt;210&gt; 325

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ANTI-CANCER (PARTICULARLY FOR SARCOMAS)

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1, 3, 5, 7, 8, 10)..(11)

&lt;223&gt; Xaa = any amino acid

&lt;400&gt; 325

Xaa Phe Xaa Asp Xaa Trp Xaa Xaa Leu Xaa Xaa  
1 5 10

&lt;210&gt; 326

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; P16-MIMETIC

&lt;400&gt; 326

Lys Ala Cys Arg Arg Leu Phe Gly Pro Val Asp Ser Glu Gln Leu Ser  
1 5 10 15

Arg Asp Cys Asp  
20

&lt;210&gt; 327

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; P16-MIMETIC

&lt;400&gt; 327

Arg Glu Arg Trp Asn Phe Asp Phe Val Thr Glu Thr Pro Leu Glu Gly  
1 5 10 15

Asp Phe Ala Trp  
20

&lt;210&gt; 328

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; P16-MIMETIC

&lt;400&gt; 328

Lys	Arg	Arg	Gln	Thr	Ser	Met	Thr	Asp	Phe	Tyr	His	Ser	Lys	Arg	Arg
1			-	5					10					15	

Leu	Ile	Phe	Ser
			20

&lt;210&gt; 329

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; P16-MIMETIC

&lt;400&gt; 329

Thr	Ser	Met	Thr	Asp	Phe	Tyr	His	Ser	Lys	Arg	Arg	Leu	Ile	Phe	Ser
1				5					10					15	

Lys	Arg	Lys	Pro
			20

&lt;210&gt; 330

&lt;211&gt; 5

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; P16-MIMETIC

&lt;400&gt; 330

Arg	Arg	Leu	Ile	Phe
1			5	

&lt;210&gt; 331

&lt;211&gt; 36

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; P16-MIMETIC

&lt;400&gt; 331

Lys	Arg	Arg	Gln	Thr	Ser	Ala	Thr	Asp	Phe	Tyr	His	Ser	Lys	Arg	Arg
1				5					10					15	

Leu	Ile	Phe	Ser	Arg	Gln	Ile	Lys	Ile	Trp	Phe	Gln	Asn	Arg	Arg	Met
			20					25					30		

Lys	Trp	Lys	Lys
			35

&lt;210&gt; 332

&lt;211&gt; 24

<212> PRT  
 <213> Artificial Sequence

<220>  
 <223> P16-MIMETIC

<400> 332

Lys Arg Arg Leu Ile Phe Ser Lys Arg Gln Ile Lys Ile Trp Phe Gln  
 1 5 10 15

Asn Arg Arg Met Lys Trp Lys Lys  
 20

<210> 333  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> PREFERRED LINKER

<400> 333

Gly Gly Gly Lys Gly Gly Gly Gly  
 1 5

<210> 334  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> PREFERRED LINKER

<400> 334

Gly Gly Gly Asn Gly Ser Gly Gly  
 1 5

<210> 335  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> PREFERRED LINKER

<400> 335

Gly Gly Gly Cys Gly Gly Gly Gly  
 1 5

<210> 336  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> PREFERRED LINKER

<400> 336

Gly Pro Asn Gly Gly  
1 5

<210> 337  
<211> 41 -  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC

<220>  
<221> misc\_feature  
<222> (1)..(1)  
<223> Fc domain attached at Position 1 of the N-terminus

<400> 337

Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala  
1 5 10 15

Ala Arg Ala Gly Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr  
20 25 30

Leu Arg Gln Trp Leu Ala Ala Arg Ala  
35 40

<210> 338  
<211> 41  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC

<220>  
<221> misc\_feature  
<222> (41)..(41)  
<223> Fc domain attached at Position 41 of the C-terminus

<400> 338

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15

Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
20 25 30

Ala Ala Arg Ala Gly Gly Gly Gly Gly  
35 40

<210> 339  
<211> 49  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> EPO-MIMETIC



<220>  
 <221> misc\_feature  
 <222> (1)..(1)  
 <223> Fc domain attached at Position 1 of the N-terminus

<400> 339

Gly Gly Gly Gly Gly Gly Gly Thr Tyr Ser Cys His Phe Gly Pro Leu  
 1 5 10 15

Thr Trp Val Cys Lys Pro Gln Gly Gly Gly Gly Gly Gly Gly Thr  
 20 25 30

Tyr Ser Cys His Phe Gly Pro Leu Thr Trp Val Cys Lys Pro Gln Gly  
 35 40 45

Gly

<210> 340  
 <211> 49  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> EPO-MIMETIC

<220>  
 <221> misc\_feature  
 <222> (49)..(49)  
 <223> Fc domain attached at Position 49 of the C-terminus

<400> 340

Gly Gly Thr Tyr Ser Cys His Phe Gly Pro Leu Thr Trp Val Cys Lys  
 1 5 10 15

Pro Gln Gly Gly Gly Gly Gly Gly Gly Thr Tyr Ser Cys His Phe  
 20 25 30

Gly Pro Leu Thr Trp Val Cys Lys Pro Gln Gly Gly Gly Gly Gly Gly  
 35 40 45

Gly

<210> 341  
 <211> 28  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDES

<400> 341

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Ile Glu  
 1 5 10 15

Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala  
20 25

<210> 342  
<211> 29  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC PEPTIDES

<400> 342

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Ile  
1 5 10 15

Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala  
20 25

<210> 343  
<211> 30  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC PEPTIDES

<400> 343

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala  
20 25 30

<210> 344  
<211> 31  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC PEPTIDES

<400> 344

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15

Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala  
20 25 30

<210> 345  
<211> 32  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC PEPTIDES

&lt;400&gt; 345

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
 1 5 10 15

Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala  
 20 25 30

&lt;210&gt; 346

&lt;211&gt; 33

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TPO-MIMETIC PEPTIDES

&lt;400&gt; 346

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
 1 5 10 15

Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg  
 20 25 30

Ala

&lt;210&gt; 347

&lt;211&gt; 34

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TPO-MIMETIC PEPTIDES

&lt;400&gt; 347

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
 1 5 10 15

Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala  
 20 25 30

Arg Ala

&lt;210&gt; 348

&lt;211&gt; 35

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TPO-MIMETIC PEPTIDES

&lt;400&gt; 348

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
 1 5 10 15

Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala  
 20 25 30

Ala Arg Ala  
 35 -

<210> 349  
 <211> 36  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDES

<400> 349

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
 1 5 10 15

Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
 20 25 30

Ala Ala Arg Ala  
 35

<210> 350  
 <211> 37  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDES

<400> 350

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
 1 5 10 15

Gly Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp  
 20 25 30

Leu Ala Ala Arg Ala  
 35

<210> 351  
 <211> 38  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDES

<400> 351

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
 1 5 10 15

Gly Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln  
 20 25 30

Trp Leu Ala Ala Arg Ala  
35

<210> 352  
<211> 42  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC PEPTIDES  
<400> 352

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro  
20 25 30

Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala  
35 40

<210> 353  
<211> 32  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC PEPTIDES  
<400> 353

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Pro  
1 5 10 15

Asn Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala  
20 25 30

<210> 354  
<211> 36  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TPO-MIMETIC PEPTIDES  
<400> 354

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15

Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
20 25 30

Ala Ala Arg Ala  
35

<210> 355  
 <211> 36  
 <212> PRT  
 <213> Artificial Sequence

<220> -  
 <223> TPO-MIMETIC PEPTIDES

<400> 355

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
 1 5 10 15

Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
 20 25 30

Ala Ala Arg Ala  
 35

<210> 356  
 <211> 36  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDES

<400> 356

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
 1 5 10 15

Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
 20 25 30

Ala Ala Arg Ala  
 35

<210> 357  
 <211> 36  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDES

<400> 357

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
 1 5 10 15

Gly Lys Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
 20 25 30

Ala Ala Arg Ala  
 35

<210> 358  
 <211> 37

<212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDES

<220>  
 <221> misc\_feature  
 <222> (19)..(19)  
 <223> Position 19, Xaa = bromoacetyl

<400> 358

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
 1 5 10 15

Gly Lys Xaa Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp  
 20 25 30

Leu Ala Ala Arg Ala  
 35

<210> 359  
 <211> 36  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDES

<400> 359

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
 1 5 10 15

Gly Cys Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
 20 25 30

Ala Ala Arg Ala  
 35

<210> 360  
 <211> 37  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDES

<220>  
 <221> misc\_feature  
 <222> (19)..(19)  
 <223> Position 19, Xaa = Poly(ethylene glycol)

<400> 360

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
 1 5 10 15

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Gly Lys Xaa Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp  
                   20                  25                  30

Leu Ala Ala Arg Ala  
                   35

<210> 361  
 <211> 37  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDES

<220>  
 <221> misc\_feature  
 <222> (19)..(19)  
 <223> Position 19, Xaa = Poly(ethylene glycol)

<400> 361

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
 1                  5                  10                  15

Gly Cys Xaa Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp  
                   20                  25                  30

Leu Ala Ala Arg Ala  
                   35

<210> 362  
 <211> 36  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDES

<400> 362

Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
 1                  5                  10                  15

Gly Asn Gly Ser Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
                   20                  25                  30

Ala Ala Arg Ala  
                   35

<210> 363  
 <211> 36  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TPO-MIMETIC PEPTIDES

<400> 363



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Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly  
1 5 10 15

Gly Cys Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
20- 25 30

Ala Ala Arg Ala  
35

<210> 364  
<211> 57  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fc-TMP

<400> 364  
aaaaaaggat cctcgagatt aagcacgagc agccagccac tgacgcagag tcggacc 57

<210> 365  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fc-TMP

<400> 365  
aaaggtggag gtggtggtat cgaaggtccg actctgcgt 39

<210> 366  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fc-TMP

<400> 366  
cagtggtcgg ctgctcgtgc ttaatctcga ggatcctttt tt 42

<210> 367  
<211> 81  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fc-TMP

<220>  
<221> CDS  
<222> (1)..(60)  
<223>

<400> 367  
aaa ggt gga ggt ggt ggt atc gaa ggt ccg act ctg cgt cag tgg ctg 48  
Lys Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
1 5 10 15

gct gct cgt gct taatctcgag gatccttttt t 81

Ala Ala Arg Ala  
20

<210> 368  
<211> 20 -  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Fc-TMP

<400> 368

Lys Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
1 5 10 15

Ala Ala Arg Ala  
20

<210> 369  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fc-TMP

<400> 369  
aacataagta cctgtaggat cg

22

<210> 370  
<211> 52  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fc-TMP

<400> 370  
ttcgatacca ccacctccac ctttaccgag agacagggag aggctcttct gc

52

<210> 371  
<211> 60  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fc-TMP-TMP

<400> 371  
aaaggtggag gtggtggtat cgaaggtccg actctgcgct agtggctggc tgctcgtgct

60

<210> 372  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fc-TMP-TMP

<400> 372  
acctccacca ccagcacgag cagccagcca ctgacgcaga gtcggacc

48

<210> 373  
 <211> 66  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Fc-TMP-TMP

<400> 373  
 ggtgggtggag gtggcggcgg aggtattgag ggcccaaccc ttcgccaatg gcttgcagca 60  
 cgcgca 66

<210> 374  
 <211> 76  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Fc-TMP-TMP

<400> 374

Ala Ala Ala Ala Ala Ala Ala Gly Gly Ala Thr Cys Cys Thr Cys Gly  
 1 5 10 15

Ala Gly Ala Thr Thr Ala Thr Gly Cys Gly Cys Gly Thr Gly Cys Thr  
 20 25 30

Gly Cys Ala Ala Gly Cys Cys Ala Thr Thr Gly Gly Cys Gly Ala Ala  
 35 40 45

Gly Gly Gly Thr Thr Gly Gly Gly Cys Cys Cys Thr Cys Ala Ala Thr  
 50 55 60

Ala Cys Cys Thr Cys Cys Gly Cys Cys Gly Cys Cys  
 65 70 75

<210> 375  
 <211> 126  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Fc-TMP-TMP

<220>  
 <221> CDS  
 <222> (1)..(126)  
 <223>

<400> 375  
 aaa ggt gga ggt ggt ggt atc gaa ggt ccg act ctg cgt cag tgg ctg 48  
 Lys Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu 15  
 1 5 10

gct gct cgt gct ggt ggt gga ggt ggc ggc gga ggt att gag ggc cca 96  
 Ala Ala Arg Ala Gly Gly Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro 30  
 20 25 30

acc ctt cgc caa tgg ctt gca gca cgc gca  
 Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala  
           35                  40

126

<210> 376  
 <211> 42  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Fc-TMP-TMP

<400> 376

Lys Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu  
   1                  5                  10                  15

Ala Ala Arg Ala Gly Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro  
           20                  25                  30

Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala  
           35                  40

<210> 377  
 <211> 39  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TMP-TMP-Fc

<400> 377

Thr Thr Thr Thr Thr Thr Cys Ala Thr Ala Thr Gly Ala Thr Cys Gly  
   1                  5                  10                  15

Ala Ala Gly Gly Thr Cys Cys Gly Ala Cys Thr Cys Thr Gly Cys Gly  
           20                  25                  30

Thr Cys Ala Gly Thr Gly Gly  
           35

<210> 378  
 <211> 48  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> TMP-TMP-Fc

<400> 378

Ala Gly Cys Ala Cys Gly Ala Gly Cys Ala Gly Cys Cys Ala Gly Cys  
   1                  5                  10                  15

Cys Ala Cys Thr Gly Ala Cys Gly Cys Ala Gly Ala Gly Thr Cys Gly  
           20                  25                  30

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Gly Ala Cys Cys Thr Thr Cys Gly Ala Thr Cys Ala Thr Ala Thr Gly  
           35                                  40                                  45

<210> 379  
 <211> 45 -  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> TMP-TMP-Fc

<400> 379  
 ctggctgctc gtgctggtgg aggcggtggg gacaaaactc acaca 45

<210> 380  
 <211> 51  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> TMP-TMP-Fc

<400> 380  
 ctggctgctc gtgctggcgg tggcggcgga gggggtggca ttgagggccc a 51

<210> 381  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> TMP-TMP-Fc

<400> 381  
 aagccattgg cgaagggttg ggcctcaat gccacccct cgcaccac cgcc 54

<210> 382  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> TMP-TMP-Fc

<400> 382  
 acccttcgcc aatggcttgc agcacgcga gggggaggcg gtggggacaa aact 54

<210> 383  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> TMP-TMP-Fc

<400> 383  
 cccaccgcct cccctgcgc gtgctgc 27

<210> 384  
 <211> 189  
 <212> DNA  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; TMP-TMP-Fc

&lt;220&gt;

&lt;221&gt; CDS -

&lt;222&gt; (10)..(180)

&lt;223&gt;

&lt;400&gt; 384

```

ttttttcat atg atc gaa ggt ccg act ctg cgt cag tgg ctg gct gct cgt      51
      Met Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg
      1              5              10

```

```

gct ggc ggt ggt ggc gga ggg ggt ggc att gag ggc cca acc ctt cgc      99
Ala Gly Gly Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg
15              20              25              30

```

```

caa tgg ctg gct gct cgt gct ggt gga ggc ggt ggg gac aaa act ctg      147
Gln Trp Leu Ala Ala Arg Ala Gly Gly Gly Gly Gly Asp Lys Thr Leu
              35              40              45

```

```

gct gct cgt gct ggt gga ggc ggt ggg gac aaa actcacaca      189
Ala Ala Arg Ala Gly Gly Gly Gly Gly Asp Lys
      50              55

```

&lt;210&gt; 385

&lt;211&gt; 57

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TMP-TMP-Fc

&lt;400&gt; 385

```

Met Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly
1              5              10              15

```

```

Gly Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp
20              25              30

```

```

Leu Ala Ala Arg Ala Gly Gly Gly Gly Gly Asp Lys Thr Leu Ala Ala
35              40              45

```

```

Arg Ala Gly Gly Gly Gly Gly Asp Lys
50              55

```

&lt;210&gt; 386

&lt;211&gt; 141

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; pAMG21

&lt;400&gt; 386

```

ctaattccgc tctcacctac caaacaatgc cccctgcaa aaaataaatt catataaaaa      60

```

```

acatacagat aaccatctgc ggtgataaat tatctctggc ggtgttgaca taaataccac      120

```

```

tggcgggtgat actgagcaca t                                          141

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<210> 387  
 <211> 55  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pAMG21

<400> 387  
 cgatttgatt ctagaaggag gaataacata tggttaacgc gttggaattc ggtac 55

<210> 388  
 <211> 872  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> GM221

<400> 388  
 ttattttcgt gcggccgcac cattatcacc gccagaggta aactagtcaa cacgcacggt 60  
 gttagatatt tatcccttgc ggtgatagat tgagcacatc gatttgattc tagaaggagg 120  
 gataatatat gagcacaaaa aagaaaccat taacacaaga gcagcttgag gacgcacgtc 180  
 gccttaaagc aatttatgaa aaaaagaaaa atgaacttgg cttatcccag gaatctgtcg 240  
 cagacaagat ggggatgggg cagtcaggcg ttggtgcttt atttaatggc atcaatgcat 300  
 taaatgctta taacgcgcga ttgcttacia aaattctcaa agttagcggt gaagaattta 360  
 gcccttcaat cgccagagaa tctacgagat gtatgaagcg gttagtatgc agccgtcact 420  
 tagaagttag tatgagtacc ctgttttttc tcatgttcag gcagggatgt tctcacctaa 480  
 gcttagaacc tttaaccaag gtgatgcgga gagatgggta agcacaacca aaaaagccag 540  
 tgattctgca ttctggcttg aggttgaagg taattccatg a gcaccaa cagggtccaa 600  
 gccaaagcttt cctgacggaa tgttaattct cgttgaccct gagcaggctg ttgagccagg 660  
 tgatttctgc atagccagac ttgggggtga tgagtttacc ttcaagaaac tgatcaggga 720  
 tagcggtcag gtgtttttac aaccactaaa cccacagtac ccaatgatcc catgcaatga 780  
 gagttgttcc gttgtgggga aagttatcgc tagtcagtgg cctgaagaga cgtttggtcg 840  
 atagactagt ggatccacta gtgtttctgc cc 872

<210> 389  
 <211> 1197  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> GM221

<400> 389  
 ggcggaaacc gacgtccatc gaatggtgca aaacctttcg cggtatggca tgatagcgcc 60  
 cggaagagag tcaattcagg gtggtgaatg tgaaaccagt aacgttatac gatgtcgag 120  
 agtatgccgg tgtctcttat cagaccgttt cccgcgtggt gaaccaggcc agccacgttt 180

## A-527.ST25.txt

ctgcgaaaaac gcgggaaaaaa gtcgaagcgg cgatggcgga gctgaattac attcccaacc 240  
 gcgtggcaca acaactggcg ggcaaacagt cgctcctgat tggcgttgcc acctccagtc 300  
 tggccctgca cgcgccgtcg caaattgtcg cggcgattaa atctcgcgcc gatcaactgg 360  
 gtgccagcgt ggtggtgtcg atggtagaac gaagcggcgt cgaagcctgt aaagcggcgg 420  
 tgcacaatct tctcgcgcaa cgcgtcagtg ggctgatcat taactatccg ctggatgacc 480  
 aggatgccat tgctgtggaa gctgcctgca ctaatgttcc ggcgttattt cttgatgtct 540  
 ctgaccagac acccatcaac agtattattt tctcccatga agacggtagc cgactgggcg 600  
 tggagcatct ggtcgcatcg ggtcaccagc aaatcgcgct gttagcgggc ccattaagtt 660  
 ctgtctcggc gcgtctgct ctggctggct ggcataaata tctcactcgc aatcaaattc 720  
 agccgatagc ggaacgggaa ggcgactgga gtgccatgtc cggttttcaa caaacatgc 780  
 aaatgctgaa tgagggcatc gttccactg cgatgctggt tgccaacgat cagatggcgc 840  
 tgggcgcaat gcgcgccatt accgagtccg ggctgcgcgt tgggtgcggat atctcggtag 900  
 tgggatacga cgataccgaa gacagctcat gttatatccc gccgttaacc accatcaaac 960  
 aggattttctg cctgctgggg caaaccagcg tggaccgctt gctgcaactc tctcagggcc 1020  
 aggcggtgaa gggcaatcag ctggtgcccg tctcactggt gaaaagaaaa accaccctgg 1080  
 cgcccaatac gcaaaccgcc tctccccgcg cgttggccga ttcattaatg cagctggcac 1140  
 gacaggtttc ccgactggaa agcggacagt aaggtaccat aggatccagg cacagga 1197

<210> 390  
 <211> 61  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Fc-EMP

<400> 390  
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 g 61

<210> 391  
 <211> 72  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Fc-EMP

<400> 391  
 cggtttgcaa acccaagtca gcgggccgaa gtggcaagag taagtacctc caccaccacc 60  
 tccacctttc at 72

<210> 392  
 <211> 57  
 <212> DNA  
 <213> Artificial Sequence



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<220>
<223>  Fc-EMP

<400>  392
gtttgcaaac cgcagggtgg cggcggcggc gccggtggta cctattcctg tcatttt      57

<210>  393
<211>  60
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Fc-EMP

<400>  393
ccaggtcagc gggccaaaat gacaggaata ggtaccaccg ccgccgccgc cgccaccctg      60

<210>  394
<211>  118
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Fc-EMP

<220>
<221>  CDS
<222>  (2)..(118)
<223>

<400>  394
t atg aaa ggt gga ggt ggt ggt gga ggt act tac tct tgc cac ttc ggc      49
Met Lys Gly Gly Gly Gly Gly Gly Gly Thr Tyr Ser Cys His Phe Gly
  1          5          10          15

ccg ctg act tgg gtt tgc aaa ccg cag ggt ggc ggc ggc ggc ggc ggt      97
Pro Leu Thr Trp Val Cys Lys Pro Gln Gly Gly Gly Gly Gly Gly Gly
  20          25          30

ggt acc tat tcc tgt cat ttt      118
Gly Thr Tyr Ser Cys His Phe
  35

<210>  395
<211>  39
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Fc-EMP

<400>  395
Met Lys Gly Gly Gly Gly Gly Gly Gly Thr Tyr Ser Cys His Phe Gly
  1          5          10          15

Pro Leu Thr Trp Val Cys Lys Pro Gln Gly Gly Gly Gly Gly Gly Gly
  20          25          30

Gly Thr Tyr Ser Cys His Phe
  35

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<210> 396  
 <211> 61  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Fc-EMP

<400> 396  
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 t 61

<210> 397  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Fc-EMP

<400> 397  
 ctaattggat ccācgagatt aaccaccctg cggtttgcaa 40

<210> 398  
 <211> 18  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Fc-EMP

<400> 398  
 Gly Glu Arg Trp Cys Phe Asp Gly Pro Leu Thr Trp Val Cys Gly Glu  
 1 5 10 15

Glu Ser

<210> 399  
 <211> 61  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Fc-EMP

<400> 399  
 agagtaagta cctccaccac cacctccacc ttaccggga gacagggaga ggctcttctg 60  
 c 61

<210> 400  
 <211> 61  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> EMP-Fc

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<400> 400  
ggcccgctga cctgggtatg taagccacaa ggggggtgggg gaggcggggg gtaatctcga 60  
g 61

<210> 401  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> EMP-Fc

<400> 401  
gatcctcgag attaccccc gcctcccca ccccttggtg gcttacatac 50

<210> 402  
<211> 118  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> EMP-Fc

<220>  
<221> CDS  
<222> (1)..(108)  
<223>

<400> 402  
gtt tgc aaa ccg cag ggt ggc ggc ggc ggc ggc ggt ggt acc tat tcc 48  
Val Cys Lys Pro Gln Gly Gly Gly Gly Gly Gly Gly Gly Thr Tyr Ser  
1 5 10 15

tgt cat ttt ggc ccg ctg acc tgg gta tgt aag cca caa ggg ggt ggg 96  
Cys His Phe Gly Pro Leu Thr Trp Val Cys Lys Pro Gln Gly Gly Gly  
20 25 30

gga ggc ggg ggg taatctcgag 118  
Gly Gly Gly Gly  
35

<210> 403  
<211> 36  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> EMP-Fc

<400> 403  
Val Cys Lys Pro Gln Gly Gly Gly Gly Gly Gly Gly Gly Thr Tyr Ser  
1 5 10 15

Cys His Phe Gly Pro Leu Thr Trp Val Cys Lys Pro Gln Gly Gly Gly  
20 25 30

Gly Gly Gly Gly  
35

<210> 404  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> EMP-Fc

<400> 404  
 ttattttcata tgaaaggtgg taactattcc tgtcatttt

39

<210> 405  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> EMP-Fc

<400> 405  
 tggacatgtg tgagttttgt cccccccgcc tccccacccc cct

43

<210> 406  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> EMP-Fc

<400> 406  
 agggggtggg ggaggcggg gggacaaaac tcacacatgt cca

43

<210> 407  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> EMP-Fc

<400> 407  
 gttattgctc agcgggtggca

20

<210> 408  
 <211> 60  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> EMP-EMP-Fc

<400> 408  
 ttttttatcg atttgattct agatttgagt ttttaactttt agaaggagga ataaaatatg

60

<210> 409  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> EMP-EMP-Fc

<400> 409  
 taaaagttaa aactcaaata tagaatcaaa tcgataaaaa a 41

<210> 410  
 <211> 51 -  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> EMP-EMP-Fc

<400> 410  
 ggaggtactt actcttgcca cttcggcccg ctgacttggg tttgcaaacc g 51

<210> 411  
 <211> 55  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> EMP-EMP-Fc

<400> 411  
 agtcagcggg ccgaagtggc aagagtaagt acctcccata ttttattcct ccttc 55

<210> 412  
 <211> 60  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> EMP-EMP-Fc

<400> 412  
 caggggtggcg gcggcggcgg cgggtggtacc tattcctgtc attttggccc gctgacctgg 60

<210> 413  
 <211> 60  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> EMP-EMP-Fc

<400> 413  
 aaaatgacag gaataggtac caccgccgcc gccgccgcca cctgcggtt tgcaaacc 60

<210> 414  
 <211> 57  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> EMP-EMP-Fc

<400> 414  
 gtatgtaagc cacaaggggg tgggggaggg gggggggaca aaactcacac atgtcca 57

<210> 415  
 <211> 60  
 <212> DNA  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; EMP-EMP-Fc

&lt;400&gt; 415

agttttgtcc cccccgcctc ccccaccccc ttgtggctta catacccagg tcagcgggcc 60

&lt;210&gt; 416

&lt;211&gt; 228

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; EMP-EMP-Fc

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (58)..(228)

&lt;223&gt;

&lt;400&gt; 416

ttttttatcg atttgattct agatttgagt ttttaactttt agaaggagga ataaaaat 57

atg gga ggt act tac tct tgc cac ttc ggc ccg ctg act tgg gtt tgc 105

Met Gly Gly Thr Tyr Ser Cys His Phe Gly Pro Leu Thr Trp Val Cys  
1 5 10 15

aaa ccg cag ggt ggc ggc ggc ggc ggc ggt ggt acc tat tcc tgt cat 153

Lys Pro Gln Gly Gly Gly Gly Gly Gly Gly Gly Thr Tyr Ser Cys His  
20 25 30

ttt ggc ccg ctg acc tgg gta tgt aag cca caa ggg ggt ggg gga ggc 201

Phe Gly Pro Leu Thr Trp Val Cys Lys Pro Gln Gly Gly Gly Gly Gly  
35 40 45

ggg ggg gac aaa act cac aca tgt cca 228

Gly Gly Asp Lys Thr His Thr Cys Pro  
50 55

&lt;210&gt; 417

&lt;211&gt; 57

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; EMP-EMP-Fc

&lt;400&gt; 417

Met Gly Gly Thr Tyr Ser Cys His Phe Gly Pro Leu Thr Trp Val Cys  
1 5 10 15Lys Pro Gln Gly Gly Gly Gly Gly Gly Gly Gly Thr Tyr Ser Cys His  
20 25 30Phe Gly Pro Leu Thr Trp Val Cys Lys Pro Gln Gly Gly Gly Gly Gly  
35 40 45Gly Gly Asp Lys Thr His Thr Cys Pro  
50 55

<210> 418  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220> -  
 <223> FC-EMP-EMP

<400> 418  
 ctaattggat cctcgagatt aaccccccttg tggcttacat

40

<210> 419  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> EPO-MIMETIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (1, 3, 9, 14, 15)..(16)  
 <223> Xaa (Positions 1, 3, 9, 14, 15 & 16) can be any one of the 20 L-amino acids

<220>  
 <221> misc\_feature  
 <222> (5)..(5)  
 <223> Xaa can be R, H, L or W

<220>  
 <221> misc\_feature  
 <222> (6)..(6)  
 <223> Xaa can be M, F or I

<220>  
 <221> misc\_feature  
 <222> (12)..(12)  
 <223> Xaa can be D, E, I, L or V

<220>  
 <221> misc\_feature  
 <222> (13)..(13)  
 <223> Xaa can be C, A, a-amino-y-bromobutyric acid or Hoc

<400> 419

Xaa Tyr Xaa Xaa Xaa Xaa Gly Pro Xaa Thr Trp Xaa Xaa Xaa Xaa Xaa  
 1 5 10 15

<210> 420  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> EPO-MIMETIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (1, 3, 5, 6, 9, 12, 14, 15)..(16)

<223> Xaa = any amino acid residue

<400> 420

Xaa Tyr Xaa Cys Xaa Xaa Gly Pro Xaa Thr Trp Xaa Cys Xaa Xaa Xaa  
1 5 10 15

<210> 421

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> EPO-MIMETIC PEPTIDE

<220>

<221> misc\_feature

<222> (2)..(2)

<223> Xaa can be R, H, L, or W

<220>

<221> misc\_feature

<222> (3)..(3)

<223> Xaa can be M, F, or I

<220>

<221> misc\_feature

<222> (6)..(6)

<223> Xaa is independently selected from any one of the 20 genetically coded L-amino acids or the stereoisomeric D-amino acids

<220>

<221> misc\_feature

<222> (9)..(9)

<223> Xaa can be D, E, I, L, or V.

<400> 421

Cys Xaa Xaa Gly Pro Xaa Thr Trp Xaa Cys  
1 5 10

<210> 422

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> EPO-MIMETIC PEPTIDE

<400> 422

Gly Gly Thr Tyr Ser Cys His Gly Pro Leu Thr Trp Val Cys Lys Pro  
1 5 10 15

Gln Gly Gly

<210> 423

<211> 19



<212> PRT  
 <213> Artificial Sequence

<220>  
 <223> EPO-MIMETIC PEPTIDE

<400> 423

Val	Gly	Asn	Tyr	Met	Ala	His	Met	Gly	Pro	Ile	Thr	Trp	Val	Cys	Arg
1				5					10					15	

Pro Gly Gly

<210> 424  
 <211> 18  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> EPO-MIMETIC PEPTIDE

<400> 424

Gly	Gly	Pro	His	His	Val	Tyr	Ala	Cys	Arg	Met	Gly	Pro	Leu	Thr	Trp
1				5					10					15	

Ile Cys

<210> 425  
 <211> 18  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> EPO-MIMETIC PEPTIDE

<400> 425

Gly	Gly	Thr	Tyr	Ser	Cys	His	Phe	Gly	Pro	Leu	Thr	Trp	Val	Cys	Lys
1				5					10					15	

Pro Gln

<210> 426  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> EPO-MIMETIC PEPTIDE

<400> 426

Gly	Gly	Leu	Tyr	Ala	Cys	His	Met	Gly	Pro	Met	Thr	Trp	Val	Cys	Gln
1				5					10					15	

Pro Leu Arg Gly  
 20

<210> 427  
 <211> 22  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> EPO-MIMETIC PEPTIDE

<400> 427

Thr Ile Ala Gln Tyr Ile Cys Tyr Met Gly Pro Glu Thr Trp Glu Cys  
 1 5 10 15

Arg Pro Ser Pro Lys Ala  
 20

<210> 428  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> EPO-MIMETIC PEPTIDE

<400> 428

Tyr Ser Cys His Phe Gly Pro Leu Thr Trp Val Cys Lys  
 1 5 10

<210> 429  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> EPO-MIMETIC PEPTIDE

<400> 429

Tyr Cys His Phe Gly Pro Leu Thr Trp Val Cys  
 1 5 10

<210> 430  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> UKR ANTAGONIST PEPTIDE

<400> 430

Ala Glu Pro Val Tyr Gln Tyr Glu Leu Asp Ser Tyr Leu Arg Ser Tyr  
 1 5 10 15

Tyr

<210> 431  
 <211> 17

<212> PRT  
 <213> Artificial Sequence

<220>  
 <223> UKR ANTAGONIST PEPTIDE

<400> 431

Ala Glu Leu Asp Leu Ser Thr Phe Tyr Asp Ile Gln Tyr Leu Leu Arg  
 1 5 10 15

Thr

<210> 432  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> UKR ANTAGONIST PEPTIDE

<400> 432

Ala Glu Phe Phe Lys Leu Gly Pro Asn Gly Tyr Val Tyr Leu His Ser  
 1 5 10 15

Ala

<210> 433  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> UKR ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (4, 5)..(6)  
 <223> Xaa = any amino acid

<400> 433

Phe Lys Leu Xaa Xaa Xaa Gly Tyr Val Tyr Leu  
 1 5 10

<210> 434  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> UKR ANTAGONIST PEPTIDE

<400> 434

Ala Glu Ser Thr Tyr His His Leu Ser Leu Gly Tyr Met Tyr Thr Leu  
 1 5 10 15

Asn

<210> 435  
 <211> 11 -  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> UKR ANTAGONIST PEPTIDE  
  
 <220>  
 <221> misc\_feature  
 <222> (3, 5)..(6)  
 <223> Xaa = any amino acid

&lt;400&gt; 435

Tyr His Xaa Leu Xaa Xaa Gly Tyr Met Tyr Thr  
 1 5 10

<210> 436  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> MAST CELL ANTAGONISTS/PROTEASE INHIBITOR PEPTIDE  
  
 <400> 436

Arg Asn Arg Gln Lys Thr  
 1 5

<210> 437  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> MAST CELL ANTAGONISTS/PROTEASE INHIBITOR PEPTIDE  
  
 <400> 437

Arg Asn Arg Gln  
 1

<210> 438  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> MAST CELL ANTAGONISTS/PROTEASE INHIBITOR PEPTIDE  
  
 <400> 438

Arg Asn Arg Gln Lys  
 1 5

<210> 439  
 <211> 5

<212> PRT  
 <213> Artificial Sequence

<220>  
 <223> MAST CELL ANTAGONISTS/PROTEASE INHIBITOR PEPTIDE  
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 <400> 439

Asn Arg Gln Lys Thr  
 1 5

<210> 440  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> MAST CELL ANTAGONISTS/PROTEASE INHIBITOR PEPTIDE  
 <400> 440

Arg Gln Lys Thr  
 1

<210> 441  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> INTEGRIN-BINDING PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (2, 5)..(7)  
 <223> Xaa = any amino acid

<400> 441

Arg Xaa Glu Thr Xaa Trp Xaa  
 1 5

<210> 442  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> INTEGRIN-BINDING PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (2, 5)..(7)  
 <223> Xaa = any amino acid

<400> 442

Arg Xaa Glu Thr Xaa Trp Xaa  
 1 5

<210> 443  
 <211> 5

<212> PRT  
 <213> Artificial Sequence

<220>  
 <223> INTEGRIN-BINDING PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (5)..(6)  
 <223> Xaa = any amino acid

<400> 443

Arg Gly Asp Gly Xaa  
 1 5

<210> 444  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> INTEGRIN-BINDING PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (6)..(6)  
 <223> Xaa = any amino acid

<400> 444

Cys Arg Gly Asp Gly Xaa Cys  
 1 5

<210> 445  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> INTEGRIN-BINDING PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (2, 3, 4, 8, 9, 10, 11, 12, 13)..(14)  
 <223> Xaa = any amino acid

<400> 445

Cys Xaa Xaa Xaa Arg Leu Asp Xaa Xaa Xaa Xaa Xaa Xaa Cys  
 1 5 10 15

<210> 446  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> INTEGRIN-BINDING PEPTIDE

<400> 446

A-527.ST25.txt  
Cys Ala Arg Arg Leu Asp Ala Pro Cys  
1 5

<210> 447  
<211> 9 -  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> INTEGRIN-BINDING PEPTIDE

<400> 447

Cys Pro Ser Arg Leu Asp Ser Pro Cys  
1 5

<210> 448  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> INTEGRIN-BINDING PEPTIDE

<220>  
<221> misc\_feature  
<222> (1, 2, 3, 7, 8)..(9)  
<223> Xaa are capable of forming a cyclizing bond

<220>  
<221> misc\_feature  
<222> (2)..(5)  
<223> Feature at 1, 5 is an amino acid capable of forming a cyclizing bond and attached to 1-5 amino acid linker

<400> 448

Xaa Xaa Xaa Arg Gly Asp Xaa Xaa Xaa  
1 5

<210> 449  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> INTEGRIN-BINDING PEPTIDE

<220>  
<221> misc\_feature  
<222> (2)..(8)  
<223> Xaa = any amino acid

<400> 449

Cys Xaa Cys Arg Gly Asp Cys Xaa Cys  
1 5

<210> 450  
<211> 9  
<212> PRT

<213> Artificial Sequence

<220>

<223> INTEGRIN-BINDING PEPTIDE

<400> 450 -

Cys Asp Cys Arg Gly Asp Cys Phe Cys  
1 5

<210> 451

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> INTEGRIN-BINDING PEPTIDE

<400> 451

Cys Asp Cys Arg Gly Asp Cys Leu Cys  
1 5

<210> 452

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> INTEGRIN-BINDING PEPTIDE

<400> 452

Cys Leu Cys Arg Gly Asp Cys Ile Cys  
1 5

<210> 453

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> INTEGRIN-BINDING PEPTIDE

<220>

<221> misc\_feature

<222> (1, 2, 5, 6, 7)..(8)

<223> Xaa = any amino acid

<400> 453

Xaa Xaa Asp Asp Xaa Xaa Xaa Xaa  
1 5

<210> 454

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> INTEGRIN-BINDING PEPTIDE

<220>



<221> misc\_feature  
 <222> (1, 2, 3, 6, 7, 8, 9)..(10)  
 <223> Xaa = any amino acid

<400> 454 -

Xaa Xaa Xaa Asp Asp Xaa Xaa Xaa Xaa Xaa  
 1 5 10

<210> 455  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> INTEGRIN-BINDING PEPTIDE

<400> 455

Cys Trp Asp Asp Gly Trp Leu Cys  
 1 5

<210> 456  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> INTEGRIN-BINDING PEPTIDE

<400> 456

Cys Trp Asp Asp Leu Trp Trp Leu Cys  
 1 5

<210> 457  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> INTEGRIN-BINDING PEPTIDE

<400> 457

Cys Trp Asp Asp Gly Leu Met Cys  
 1 5

<210> 458  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> INTEGRIN-BINDING PEPTIDE

<400> 458

Cys Trp Asp Asp Gly Trp Met Cys  
 1 5

<210> 459

<211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> INTEGRIN-BINDING PEPTIDE

<400> 459

Cys Ser Trp Asp Asp Gly Trp Leu Cys  
 1 5

<210> 460  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> INTEGRIN-BINDING PEPTIDE

<400> 460

Cys Pro Asp Asp Leu Trp Trp Leu Cys  
 1 5

<210> 461  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> EPO-MIMETIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (2)..(8)  
 <223> Xaa can be any of the 20 L-amino acids

<220>  
 <221> misc\_feature  
 <222> (3)..(3)  
 <223> Xaa can be C, A, a-amino-y-bromobutyric acid or Hoc

<220>  
 <221> misc\_feature  
 <222> (4)..(4)  
 <223> Xaa can be R, H, L or W

<220>  
 <221> misc\_feature  
 <222> (5)..(5)  
 <223> Xaa can be M, F or I; Xaa

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> Xaa can be D, E, I, L or V

<220>  
 <221> misc\_feature  
 <222> (12)..(12)

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<223> Xaa can be C, A, a-amino-γ-bromobutyric acid or Hoc; provided that Xaa (Pos3 or 12) is C or Hoc.

<400> 461

Tyr Xaa Xaa Xaa Xaa Gly Pro Xaa Thr Trp Xaa Xaa  
1 5 10

<210> 462

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> SELECTIN ANTAGONIST PEPTIDE

<400> 462

Cys Gln Asn Arg Tyr Thr Asp Leu Val Ala Ile Gln Asn Lys Asn Glu  
1 5 10 15

<210> 463

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> SELECTIN ANTAGONIST PEPTIDE

<400> 463

Ala Glu Asn Trp Ala Asp Asn Glu Pro Asn Asn Lys Arg Asn Asn Glu  
1 5 10 15

Asp

<210> 464

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> SELECTIN ANTAGONIST PEPTIDE

<400> 464

Arg Lys Asn Asn Lys Thr Trp Thr Trp Val Gly Thr Lys Lys Ala Leu  
1 5 10 15

Thr Asn Glu

<210> 465

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> SELECTIN ANTAGONIST PEPTIDE

&lt;400&gt; 465

Lys Lys Ala Leu Thr Asn Glu Ala Glu Asn Trp Ala Asp  
 1 5 10

<210> 466  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SELECTIN ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (3)..(15)  
 <223> Xaa = any amino acid

&lt;400&gt; 466

Cys Gln Xaa Arg Tyr Thr Asp Leu Val Ala Ile Gln Asn Lys Xaa Glu  
 1 5 10 15

<210> 467  
 <211> 19  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SELECTIN ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (3, 5, 6, 13)..(15)  
 <223> Xaa = any amino acid

&lt;400&gt; 467

Arg Lys Xaa Asn Xaa Xaa Trp Thr Trp Val Gly Thr Xaa Lys Xaa Leu  
 1 5 10 15

Thr Glu Glu

<210> 468  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SELECTIN ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (13)..(15)  
 <223> Xaa = any amino acid

&lt;400&gt; 468

Ala Glu Asn Trp Ala Asp Gly Glu Pro Asn Asn Lys Xaa Asn Xaa Glu  
 1 5 10 15

Asp

<210> 469  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SELECTIN ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (2, 3, 4, 7)..(15)  
 <223> Xaa = any amino acid

<400> 469

Cys Xaa Xaa Xaa Tyr Thr Xaa Leu Val Ala Ile Gln Asn Lys Xaa Glu  
 1 5 10 15

<210> 470  
 <211> 19  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SELECTIN ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (3, 4, 5, 6, 8, 13, 15)..(18)  
 <223> Xaa = any amino acid

<400> 470

Arg Lys Xaa Xaa Xaa Xaa Trp Xaa Trp Val Gly Thr Xaa Lys Xaa Leu  
 1 5 10 15

Thr Xaa Glu

<210> 471  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SELECTIN ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (2, 5, 6, 7, 12, 13)..(14)  
 <223> Xaa = any amino acid

<400> 471

Ala Xaa Asn Trp Xaa Xaa Xaa Glu Pro Asn Asn Xaa Xaa Xaa Glu Asp  
 1 5 10 15

<210> 472  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SELECTIN ANTAGONIST PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (1, 3, 6, 9, 12)..(13)  
 <223> Xaa = any amino acid

<400> 472

Xaa Lys Xaa Lys Thr Xaa Glu Ala Xaa Asn Trp Xaa Xaa  
 1 5 10

<210> 473  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (1)..(1)  
 <223> Xaa is Asp-Arg-Met-Pro-Cys, Arg-Met-Pro-Cys, Met-Pro-Cys, Pro-Cys  
 or Cys

<220>  
 <221> misc\_feature  
 <222> (2)..(2)  
 <223> Xaa is Arg or Lys

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Xaa is Ser or Thr

<220>  
 <221> misc\_feature  
 <222> (12)..(12)  
 <223> Xaa is Cys-Lys or Cys

<400> 473

Xaa Xaa Asn Phe Phe Trp Lys Thr Phe Xaa Ser Xaa  
 1 5 10

<210> 474  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE

&lt;400&gt; 474

Asp Arg Met Pro Cys Arg Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys  
 1 5 10 15

Lys

&lt;210&gt; 475

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE

&lt;400&gt; 475

Met Pro Cys Arg Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys  
 1 5 10 15

&lt;210&gt; 476

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE

&lt;400&gt; 476

Cys Arg Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys  
 1 5 10

&lt;210&gt; 477

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE

&lt;400&gt; 477

Asp Arg Met Pro Cys Arg Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys  
 1 5 10 15

&lt;210&gt; 478

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE

&lt;400&gt; 478

Met Pro Cys Arg Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys  
 1 5 10

&lt;210&gt; 479

<211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE

<400> 479

Cys Arg Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys  
 1 5 10

<210> 480  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE

<400> 480

Asp Arg Met Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys  
 1 5 10 15

<210> 481  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE

<400> 481

Met Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys  
 1 5 10 15

<210> 482  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE

<400> 482

Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys  
 1 5 10

<210> 483  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE

<400> 483

Asp Arg Met Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys  
 1 5 10 15



<210> 484  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE  
 <400> 484

Met Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys  
 1 5 10

<210> 485  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE  
 <400> 485

Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys  
 1 5 10

<210> 486  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE  
 <400> 486

Asp Arg Met Pro Cys Arg Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys  
 1 5 10 15

Lys

<210> 487  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE  
 <400> 487

Met Pro Cys Arg Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys Lys  
 1 5 10 15

<210> 488  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE  
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&lt;400&gt; 488

Cys	Arg	Asn	Phe	Phe	Trp	Lys	Thr	Phe	Thr	Ser	Cys	Lys
1				5					10			

&lt;210&gt; 489

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE

&lt;400&gt; 489

Asp	Arg	Met	Pro	Cys	Arg	Asn	Phe	Phe	Trp	Lys	Thr	Phe	Thr	Ser	Cys
1				5					10					15	

&lt;210&gt; 490

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE

&lt;400&gt; 490

Met	Pro	Cys	Arg	Asn	Phe	Phe	Trp	Lys	Thr	Phe	Thr	Ser	Cys
1				5					10				

&lt;210&gt; 491

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE

&lt;400&gt; 491

Cys	Arg	Asn	Phe	Phe	Trp	Lys	Thr	Phe	Thr	Ser	Cys
1				5					10		

&lt;210&gt; 492

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE

&lt;400&gt; 492

Asp	Arg	Met	Pro	Cys	Lys	Asn	Phe	Phe	Trp	Lys	Thr	Phe	Thr	Ser	Cys
1				5					10					15	

Lys

&lt;210&gt; 493

<211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE

<400> 493

Met	Pro	Cys	Lys	Asn	Phe	Phe	Trp	Lys	Thr	Phe	Thr	Ser	Cys	Lys
1				5					10					15

<210> 494  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE

<400> 494

Cys	Lys	Asn	Phe	Phe	Trp	Lys	Thr	Phe	Thr	Ser	Cys	Lys
1				5					10			

<210> 495  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE

<400> 495

Asp	Arg	Met	Pro	Cys	Lys	Asn	Phe	Phe	Trp	Lys	Thr	Phe	Thr	Ser	Cys
1				5					10					15	

<210> 496  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE

<400> 496

Met	Pro	Cys	Lys	Asn	Phe	Phe	Trp	Lys	Thr	Phe	Thr	Ser	Cys
1				5					10				

<210> 497  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SOMATOSTATIN OR CORTISTATIN MIMETIC PEPTIDE

<400> 497

Cys	Lys	Asn	Phe	Phe	Trp	Lys	Thr	Phe	Thr	Ser	Cys
1				5					10		

<210> 498  
 <211> 25  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> CAP37 MIMETIC/LPS BINDING

<400> 498

Asn Gln Gly Arg His Phe Cys Gly Gly Ala Leu Ile His Ala Arg Phe  
 1 5 10 15

Val Met Thr Ala Ala Ser Cys Phe Gln  
 20 25

<210> 499  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> CAP37 MIMETIC/LPS BINDING

<400> 499

Arg His Phe Cys Gly Gly Ala Leu Ile His Ala Arg Phe Val Met Thr  
 1 5 10 15

Ala Ala Ser Cys  
 20

<210> 500  
 <211> 27  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> CAP37 MIMETIC/LPS BINDING

<400> 500

Gly Thr Arg Cys Gln Val Ala Gly Trp Gly Ser Gln Arg Ser Gly Gly  
 1 5 10 15

Arg Leu Ser Arg Phe Pro Arg Phe Val Asn Val  
 20 25

<210> 501  
 <211> 18  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> VEGF- ANTAGONIST

<400> 501

Gly Glu Arg Trp Cys Phe Asp Gly Pro Arg Ala Trp Val Cys Gly Trp  
 1 5 10 15

Glu Ile

<210> 502 -  
 <211> 18  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> VEGF- ANTAGONIST

&lt;400&gt; 502

Glu Glu Leu Trp Cys Phe Asp Gly Pro Arg Ala Trp Val Cys Gly Tyr  
 1 5 10 15

Val Lys

<210> 503  
 <211> 33  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ANTIPATHOGENIC PEPTIDE

&lt;400&gt; 503

Gly Phe Phe Ala Leu Ile Pro Lys Ile Ile Ser Ser Pro Leu Phe Lys  
 1 5 10 15

Thr Leu Leu Ser Ala Val Gly Ser Ala Leu Ser Ser Ser Gly Gly Gln  
 20 25 30

Gln

<210> 504  
 <211> 33  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ANTIPATHOGENIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (7, 18,)...(19)  
 <223> Positions 7, 18, and 19, D amino acid residue

&lt;400&gt; 504

Gly Phe Phe Ala Leu Ile Pro Lys Ile Ile Ser Ser Pro Leu Phe Lys  
 1 5 10 15

Thr Leu Leu Ser Ala Val Gly Ser Ala Leu Ser Ser Ser Gly Gly Gln  
 20 25 30

Glu

<210> 505 -  
 <211> 22  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ANTIPATHOGENIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (18)..(19)  
 <223> Positions 18 and 19, D amino acid residues

<400> 505

Gly Phe Phe Ala Leu Ile Pro Lys Ile Ile Ser Ser Pro Leu Phe Lys  
 1 5 10 15

Thr Leu Leu Ser Ala Val  
 20

<210> 506  
 <211> 22  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ANTIPATHOGENIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (7, 18)..(19)  
 <223> Positions 7, 18 and 19, D amino acid residues

<400> 506

Gly Phe Phe Ala Leu Ile Pro Lys Ile Ile Ser Ser Pro Leu Phe Lys  
 1 5 10 15

Thr Leu Leu Ser Ala Val  
 20

<210> 507  
 <211> 23  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ANTIPATHOGENIC PEPTIDE

<220>  
 <221> misc\_feature  
 <222> (8, 19)..(20)  
 <223> Positions 8, 19 and 20, D amino acid residues

<400> 507

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Lys Gly Phe Phe Ala Leu Ile Pro Lys Ile Ile Ser Ser Pro Leu Phe  
1 5 10 15

Lys Thr Leu Leu Ser Ala Val  
20

<210> 508  
<211> 24  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> ANTIPATHOGENIC PEPTIDE

<220>  
<221> misc\_feature  
<222> (9, 20)..(21)  
<223> Positions 9, 20 and 21, D amino acid residues

<400> 508

Lys Lys Gly Phe Phe Ala Leu Ile Pro Lys Ile Ile Ser Ser Pro Leu  
1 5 10 15

Phe Lys Thr Leu Leu Ser Ala Val  
20

<210> 509  
<211> 24  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> ANTIPATHOGENIC PEPTIDE

<220>  
<221> misc\_feature  
<222> (9, 20)..(21)  
<223> Positions 9, 20 and 21, D amino acid residues

<400> 509

Lys Lys Gly Phe Phe Ala Leu Ile Pro Lys Ile Ile Ser Ser Pro Leu  
1 5 10 15

Phe Lys Thr Leu Leu Ser Ala Val  
20

<210> 510  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> ANTIPATHOGENIC PEPTIDE

<220>  
<221> misc\_feature  
<222> (7)..(7)

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<223> Position 7, D amino acid residue

<400> 510

Gly Phe Phe Ala Leu Ile Pro Lys Ile Ile Ser  
1 5 10

<210> 511  
<211> 26  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> ANTIPATHOGENIC PEPTIDE

<400> 511

Gly Ile Gly Ala Val Leu Lys Val Leu Thr Thr Gly Leu Pro Ala Leu  
1 5 10 15

Ile Ser Trp Ile Lys Arg Lys Arg Gln Gln  
20 25

<210> 512  
<211> 26  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> ANTIPATHOGENIC PEPTIDE

<220>  
<221> misc\_feature  
<222> (5, 8, 17)..(23)  
<223> Positions 5, 8, 17 and 23, D amino acid residues

<400> 512

Gly Ile Gly Ala Val Leu Lys Val Leu Thr Thr Gly Leu Pro Ala Leu  
1 5 10 15

Ile Ser Trp Ile Lys Arg Lys Arg Gln Gln  
20 25

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<223> Positions 5, 18, 17 and 23, D amino acid residues

<400> 513

Gly Ile Gly Ala Val Leu Lys Val Leu Thr Thr Gly Leu Pro Ala Leu  
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1 5 15

Ile Ser Trp Ile Lys Arg Lys Arg Gln Gln  
20 25

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Ile Ser Trp Ile Lys Arg  
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Ala Val Leu Lys Val Leu Thr Thr Gly Leu Pro Ala Leu Ile Ser Trp  
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Ile Lys Arg

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<222> (3, 4, 8)..(10)  
<223> Positions 3, 4, 8 and 10, D amino acid residues

&lt;400&gt; 516

Lys Leu Leu Leu Leu Leu Lys Leu Leu Leu Leu Lys  
 1 5 10

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&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (3, 4, 8)..(10)

&lt;223&gt; Positions 3, 4, 8 and 10, D amino acid residues

&lt;400&gt; 517

Lys Leu Leu Leu Lys Leu Leu Leu Lys Leu Leu Lys  
 1 5 10

&lt;210&gt; 518

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

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&lt;223&gt; ANTIPATHOGENIC PEPTIDE

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (3, 4, 8)..(10)

&lt;223&gt; Positions 3, 4, 8 and 10, D amino acid residues

&lt;400&gt; 518

Lys Leu Leu Leu Lys Leu Lys Leu Lys Leu Leu Lys  
 1 5 10

&lt;210&gt; 519

&lt;211&gt; 12

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&lt;400&gt; 519

Lys Lys Leu Leu Lys Leu Lys Leu Lys Leu Lys Lys  
 1 5 10

&lt;210&gt; 520

&lt;211&gt; 12

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&lt;211&gt; 12

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&lt;400&gt; 527

Lys Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Lys  
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Lys Ile Pro Ile Lys Ile Lys Ile Lys Ile Val Lys  
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